

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 22:18:26 ; Search time 11328 Seconds  
(without alignments)  
13351.596 Million cell updates/sec

Title: US-09-700-843-1  
Perfect score: 11206  
Sequence: 1 catgatgaataacataagg.....cacgatgagaatggccagac 11206

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_estl:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_gss:*
13:	em_gss_hum:*
14:	em_gss_inv:*
15:	em_gss_pln:*
16:	em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1047.6	9.3	1070	9	AJ281552	AJ281552 4A3A-P6F1
2	984.8	8.8	1013	10	BM438846	BM438846 IpLvr0015
3	887	7.9	1004	9	AJ281480	AJ281480 4A3A-P4G8
4	874.2	7.8	935	10	BG838279	BG838279 Gc01_10e0
5	839.4	7.5	841	9	AL042026	AL042026 DKFZp434E
6	823	7.3	854	10	BM438950	BM438950 IpLvr0049
7	742	6.6	832	10	BG923768	BG923768 602825893
8	732.8	6.5	800	9	AJ281449	AJ281449 4A3A-P4D5
9	727	6.5	842	10	BI687610	BI687610 603312586
10	714.2	6.4	792	10	BI687057	BI687057 603312478
11	674.6	6.0	757	12	AQ856202	AQ856202 nbcb0001F
12	671.6	6.0	754	10	BG920379	BG920379 602826032
13	669.4	6.0	693	9	AL598527	AL598527 DKFZp3130
14	659.2	5.9	723	12	AG107786	AG107786 Pan trogl
15	656.2	5.9	675	9	AL645322	AL645322 AL645322
16	654.2	5.8	717	12	AG096290	AG096290 Pan trogl
17	651.2	5.8	711	12	AG010947	AG010947 Homo sapi

C	18	649	5.8	767	9	AL040542	AL040542 DKFZp434I
	19	648.2	5.8	672	9	AL640799	AL640799 AL640799
	20	647.2	5.8	671	9	AL660035	AL660035 AL660035
	21	644.6	5.8	670	9	AL642581	AL642581 AL642581
	22	644.2	5.7	857	12	AQ875013	AQ875013 V120B8 mT
C	23	642.6	5.7	793	12	AG000364	AG000364 Homo sapi
C	24	641.4	5.7	721	12	AG011001	AG011001 Homo sapi
C	25	638.2	5.7	702	12	AG100046	AG100046 Pan trogl
	26	636.6	5.7	651	9	AL660958	AL660958 AL660958
	27	635.2	5.7	658	9	AL656146	AL656146 AL656146
C	28	635	5.7	688	9	AL042640	AL042640 DKFZp434M
C	29	634.6	5.7	718	12	AG105206	AG105206 Pan trogl
	30	633.6	5.7	668	9	AL637190	AL637190 AL637190
	31	633.6	5.7	850	12	AQ875052	AQ875052 V120F5 mT
	32	631.8	5.6	798	12	AQ876139	AQ876139 V133G10 m
C	33	631.2	5.6	695	12	AG109026	AG109026 Pan trogl
C	34	630.2	5.6	692	12	AG089716	AG089716 Pan trogl
C	35	626.2	5.6	739	12	AG095990	AG095990 Pan trogl
	36	625.2	5.6	861	12	AQ875040	AQ875040 V120E4 mT
C	37	624.6	5.6	687	12	AG104968	AG104968 Pan trogl
	38	624	5.6	815	12	AQ876134	AQ876134 V133F5 mT
	39	623.4	5.6	718	9	AL631067	AL631067 AL631067
C	40	619.6	5.5	672	12	AG088034	AG088034 Pan trogl
C	41	619.6	5.5	699	12	AG101212	AG101212 Pan trogl
	42	619.6	5.5	799	12	AQ876220	AQ876220 V152G7 mT
	43	618.6	5.5	888	10	BI684711	BI684711 603307057
	44	618.4	5.5	784	12	AQ876152	AQ876152 V133H12 m
C	45	618.2	5.5	684	12	AG112516	AG112516 Pan trogl

ALIGNMENTS

RESULT 1

AJ281552

LOCUS

DEFINITION

AJ281552 1070 bp mRNA linear EST 30-JUN-2000

4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles

gambiae cDNA clone 4A3A-P6F11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

source

Contact: Dimopoulos G  
Fotis C. Kafatos laboratory  
European Molecular Biology Laboratory  
Meyerhofstrasse 1, 69117 Heidelberg, Germany.  
Location/Qualifiers  
1. .1070  
/organism="Anopheles gambiae"  
/strain="4A r/r"  
/db\_xref="taxon:7165"  
/clone="4A3A-P6F11"  
/clone\_lib="Anopheles gambiae immune competent 4A3A"  
/cell\_line="immune competent 4A3A"  
/lab\_host="E. coli DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: EcoRI; Site\_2: NotI; sequenced from  
forward priming site which reads from the 3' end of the  
cDNA. The 4A3A is a directionally cloned and normalized  
cDNA library that was constructed from the 4A3A cell line











VERSION	AL042026.1	GI:5421372
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 841)	
TITLE	Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.	
JOURNAL	EST (Poustka, et al.)	
COMMENT	Unpublished (1999) Contact: Poustka A.J. Department Lehrach Max-Planck-Institute for Molecular Genetics Innestrasse 73, 14195 Berlin, Germany Tel: +49-30-84131623 Fax: +49-30-84131128 Email: poustka@mping-berlin-dahlem.mpg.de This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available. This clone (DKFZp434E11) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.	

		Query Match	7.5%; Score 839.4; DB 9;	Length 841;
		Best Local Similarity	99.9%; Pred. No. 1.1e-172;	
		Matches 840; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;
QY	9554	tggcccaagtgtgcaatgatataaccgcgagacccacgctcacccggtccagatttatcagc	9613	
DG	841	TGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTACCGGCTCCAGATTATCAGC	782	
QY	9614	aataaacaccagccagccggaaggccgagcgagaaagtgtcctgcaacttttatccgcctc	9673	
DG	781	AATAAACACCAGCCAGCCGGAAGGCCGAGCGCAGAACTGGTGCTGCAACTTTATCCGCCTC	722	
QY	9674	catccagtcctattaattgttgcgcgggaagctagagtaagtagttcgcccagtaaatttt	9733	
DG	721	CATCCAGTCATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTT	662	
QY	9734	gcgcaacgttgttgccattgctacaggcatcgtgggtgcacgctcgctggttggatatgcc	9793	
DG	661	GCGCAACGTGTGTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTCTGTTGGTATGGC	602	
QY	9794	ttcattcagctccgggttccccaaagatcaaaggcgagttacatgatcccccatggtgtgcaa	9853	
DG	601	TTCATTTACGCTCCGGTTCCCACAGCATCAAGCGAGTTACATGATCCCCCATGTTGTGCAA	542	
QY	9854	aaaagcggttagctccttcggttcctccgatacgttgbtcagaagtaagttbgccgcagtggtt	9913	
DG	541	AAAAGCGGTTAGCTCCTTCGGTCTCTCCGATCGTTGTCTAGAAGTAAGTTGGCCCGCAGTGT	482	
QY	9914	atcactcatgggttatggcagcaactgcataaattctctactgtcatgccatccgtaagatg	9973	
DG	481	ATCACTCATGGTTATGGCAGCACTGCATAATTCTCTACTGTTCATGCCATCCGTAAGATG	422	

QY	9974	ctttctgtgactggtgagtaactcaaccaagtcaattcttgagaatagtgatgcggcgacc	10033
Db	421	CTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATCTGAGAAATAGTGTATCGCGCGACC	362
QY	10034	gagttgctcttgcgcggcgtcaaacacgggataataaccgcccacatagcagaactttaaa	10093
Db	361	GAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAA	302
QY	10094	agtgciccatcattggaaaaacgcttcttcggggcgaaaaactctcaaggatcttaccgctgtt	10153
Db	301	AGTGCTCATCATTTGGAAAACGTTCTTCGGGGCGGAAAACCTCTCAAGGATCTTACCGCTGTT	242
QY	10154	gagatccagttcgaatgtaaccactcgtgcaccccaactgatcttcagcatcttttactttt	10213
Db	241	GAGATCCAGTTCGATGTAAACCACTCGTGCACCCCACTGATCTTCAGCATCTTTTACTTT	182
QY	10214	caccagcgttctcgtggtgagcaaaaaacaggaagcgaataatccgcaaaaaagggaataag	10273
Db	181	CACCAAGCGTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGAATAAG	122
QY	10274	ggcgacacgggaaatgttgaaataactcatactcttctcttttcaatatattatgaagcattta	10333
Db	121	GGCGACACGGAAATGTTGAATACTCATACTCTTCTCTTTTCAATATTATTGAAGCATTTA	62
QY	10334	tcagggttattgtctcatgagcggatcacatatatttgaatgtatttagaaaaataacacaaat	10393
Db	61	TCAGGGTAAATGTTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACCAAT	2
QY	10394	a	10394
Db	1	A	1
RESULT	6		
BM438950/c			
LOCUS			
DEFINITION	BM438950	854 bp	linear EST 31-JAN-2002
	IPLVR00491	Liver cDNA library Ictalurus punctatus cDNA 5', mRNA	
		sequence.	
ACCESSION	BM438950		
VERSION	BM438950.1	GI:18460672	
KEYWORDS	EST.		
SOURCE	channel catfish.		
ORGANISM	Ictalurus punctatus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;		
	Ictaluridae; Ictalurus.		
REFERENCE	1 (bases 1 to 854)		
AUTHORS	Feng J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.		
TITLE	Transcriptome of channel catfish (Ictalurus punctatus): initial		
	analysis of expressed sequence tags from the liver		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Liu ZJ		
	The Fish Molecular Genetics and Biotechnology Laboratory,		
	Department of Fisheries and Allied Aquacultures and Program of Cell		
	and Molecular Biosciences		
	Auburn University		
	203 Swingle Hall, Auburn University, Auburn, AL 36849, USA		
	Tel: 334 844 4054		
	Fax: 334 844 9208		
	Email: zliu@acesag.auburn.edu		
	Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers		
Source	1..854		
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	/db_xref="taxon:7998"		
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	/note="Organ: Liver; Vector: pSport1; Site_1: NotI;		
	Site_2: SalI"		
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ORIGIN			

Query Match 7.3%; Score 823; DB 10; Length 854;

Best Local Similarity 99.2%; Pred. No. 4.4e-169;		Matches 848; Conservative 0; Mismatches 5; Indels 2; Gaps 2;	
QY	9402	tcaatctaaaagtatatatagagtaaacttggtctgacagttaccaaatgcttaataatcagtgag	9461
Db	854	TCATCTCAAGCATATATAGATAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAG	795
QY	9462	gcacctatctcagcgatctgtctctatttcgtttccatccocatagttgcctgactccccgtctgtg	9521
Db	794	GCACCTATCTCAGCGATCTGTCTATCTCGTTTCATCCATAGTTGCCTGACTCCCGTCGTG	735
QY	9522	tagataactacgatacgggagggttaccatctgccccagtgctgcaatgataccgcga	9581
Db	734	TAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCCGGA	675
QY	9582	gacccacgctcacggctccagatttatcagcaataaaccagccagccggaaggccgag	9641
Db	674	GACCCACGCTCACCGCTCCAGATTATTCAGCAATAAACAGCCAGCCGGAAGGCCGAG	615
QY	9642	cgcagaagtggctctgcaacttttatccgcctccatccagctctattaatgttgcgggaa	9701
Db	614	CGCAGAAGTGGTCTCGCAACTTTATCCGCCCTCCATCCAGTCTATTAATTGTGCCGGAA	555
QY	9702	gctagagtaagtagttcgccagtttaataagtttgcgcaacgttgttgcattgctacagcg	9761
Db	554	GCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGC	495
QY	9762	atcgttggtgcacgctcgctggttggtatggcttcattcagctccggttccccaacgatca	9821
Db	494	ATCGTGGTGTACCGCTCGTCTGTTTGGATGGCTTCATTTCAGCTCCGTTCCCAACGATCA	435
QY	9822	aggcgagttacatgatcccccatgttgtgcaaaaaagggttagctccttcggtcctccg	9881
Db	434	AGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCT-CTCGGTCCTCCG	376
QY	9882	atcgttggtcagaagtaagtggccgcagtggttatcactcatggttatggcagcactgcat	9941
Db	375	ATCGTTGTCAGAAGTAAGTTGGCCGCASTGTTATCACTCATGTTTATGGCAGCACTGCAT	316
QY	9942	aattcttactgtcatgccatccgtaagatgcttttctgtgactggtgagtactcaacc	10001
Db	315	AATCTCTTACTGTTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGACTACTCAAC	256
QY	10002	aagtcattctgagaaatagtgatgcggcgaccgagttgctcttgcggcggtcaacacgg	10061
Db	255	AAGTCATTCTGAGATAGTGTATGCGGGCACCGAGTTGCTCTTGCCCGCGTCAATACGG	196
QY	10062	gataataccgcgcacatagcagaactttaaaagtgctcatcattggaaaacggttcttcg	10121
Db	195	GATAATACCGGCCACATAGCAGAACTTAAAGTGCTCATCATTTGGAAAAACGTTCTTCG	136
QY	10122	ggcgaaaaactctcaaggatctttacgcgtgttgagatccagttcgatgtaa-cccactcg	10180
Db	135	GGCGAAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAAGCCCACTCG	76
QY	10181	tgcacccaactgatcttcagcatcttttactttcaccaagcggtttctgggtgagcaaaaac	10240
Db	75	TGCACCCAAC TGATCTTCAGCATCTTTACTTTTACCACGGTATCTGGGTGAGCAAAAAC	16
QY	10241	aggaaggcaaaatgc 10255	
Db	15	AGGAAGGCAAAATGC 1	
RESULT	7		
LOCUS	BC923768		
DEFINITION	602825893F1 NCI_CGAP_Mam6 Mus musculus cdna clone	linear	EST 05-JUN-2001
ACCESSION	BC923768		
VERSION	BC923768.1	GI:14304244	
KEYWORDS	EST.		
	house mouse.		

ORGANISM	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 832)	
REFERENCE	NIH-MGC	http://mgc.nci.nih.gov/.	
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	
TITLE	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	
JOURNAL	Tissue Procurement: Jeffrey Green M.D.	cdNA Library Preparation: Life Technologies, Inc.	
COMMENT	DNA Sequencing by: Incyte Genomics, Inc.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
	Plate: LLAM10915	row: j	column: 23
	High quality sequence start: 32	High quality sequence stop: 823.	
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	/dev_stage="5 months"		
	/lab_host="DH10B"		
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"		
BASE COUNT	201 a	209 c	196 g 226 t
ORIGIN			
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	Best Local Similarity	99.1%;	Pred. No. 2.3e-151;
	Matches 767;	Conservative 0;	Mismatches 5; Indels 2; Gaps 2;
QY	9357	aggatcttcacctagatccttttaaataaaaaagaagtttaaataatcaatcaagata	9416
Db	33	AGGATCTTCGGCGAGATCCTTTAAATTAATAATGAGGTTTAAATCAATCAATAAGTATA	92
QY	9417	tatagtaaaacttggctgacagttaccaatgcttaatcagtgaggcacctatctcagcg	9476
Db	93	TATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCG	152
QY	9477	atctgtctattctgttccatccatagttgcctgactccccgctgtagataaactacgata	9536
Db	153	ATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTTAGATAACTACGATA	212
QY	9537	cggagggcttacccatctggccccagtgctgcaatgataccgcgagacccacgctcaccg	9596
Db	213	CGGAGGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCG	272
QY	9597	gctccagatttatcagcaataaaccagccagccggaaggccgagcgagagtggtcct	9656
Db	273	GCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGGCCGAGAGTGGTCTCT	332
QY	9657	gcaactttatccgcctccatccagttctattaatgttgcggggaagctagagtaagtagt	9716
Db	333	GCAACTTTATCCGCCCTCCATCCAGTCTATTAATTGTTCCGGGAAGCTAGAGTAAGTAGT	392
QY	9717	tcgcagtgtaatagtttgcgcaacgttgttgccattgtctacaggcacgtcggtgtcacgc	9776
Db	393	TCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACACGC	452
QY	9777	tcgtcgtttggtatggtcttcattcagctcccggttccccaacgatcaaggcgaggttacatga	9836
Db	453	TCGTCTGTTTGGTATGSGCTTCATTCAGTCTCCGTTCCCAACCATCAAGGCGAGTTACATGA	512

QY	9837	tcgccatgtgtgcacaaagcggtttagctccttcggctcctccgatcgttgtcagaagt	9896
Db	513	TCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTGTGAGAAGT	572
QY	9897	aagtggccgcagtggtatacactcatggttatggcagcactgcataattcttactgtc	9956
Db	573	AAGTTGGCCGCAGTGTATCACTCATGTGTTATGGCAGCACTGCATAATTCTCTACTGTC	632
QY	9957	atgccatccgtaagatgctttctgtgactggtgagtactcaaccaagtcattctgagaa	10016
Db	633	ATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAATTCTGAGAA	692
QY	10017	tagtgtatcgggcg-accgagttgctcttgcgccggcggtcaacacgggataataccgcgcc	10075
Db	693	TAGTGATGCGGCGAACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCGCGCC	752
QY	10076	acatagcagaactttaaaagtgcctcatcattggaaaaacgttcttcggggcgaaa	10129
Db	753	ACATAGCAGAACTTT-AAAGTGCTCATCATTTGGAAACGTTCTTCGGGGCGGAAA	805
RESULT 8			
AJ281449			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
COMMENT			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			

QY	8662	agttcaagaagaagcgctttttccataggctccgcccccttgacgagcatcacaaaaatc	8721
Db	49	AGGCCGGCTGTGCTGGCGTTTTCCTATAGGCTCCGCCCCCTTGACGAGCATCACAAAAATA	108
QY	8722	gacgctcaagtcagaggtggcgaaacccgcagaggactataaagataccaggcgtttcccc	8781
Db	109	GACGCTCAAGTCAGAGGTGGCGAAACCCGCACAGGACTATAAAGATACCAGGCGTTTCCCC	168
QY	8782	ctggaagctccctcgtgcgctctcctgttccgacccctgcgcgttaccggataacctgtcgc	8841
Db	169	CTGGAAGCTCCCTCGTGCCTCTCCTGTCCGACCCCTGCCGTTACCGGATACCTGTCCG	228
QY	8842	cctttctcccttcgggaaagcgtggcgcttctctcaatgctcacgcgtgtaggtatctcagtt	8901
Db	229	CCTTCTCCCTTCGGGAAGCGTGGCGCTTTCCTCATAGCTACGCTGCTAGGTATCTCAGTT	288
QY	8902	cggtgtaggtcgttcgctccaagctggcgctgtgtgcacgaaccccccggttcagcccgacc	8961
Db	289	CGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGACC	348
QY	8962	gctgcgcccttatccgggtaactatcgtcttgagtcgaaccccggtgaagacacgacttatcgc	9021
Db	349	GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACAGACTTATCGC	408
QY	9022	cactggcagcagccactgggtaacaggattagcagagcgaggtatgttagcggtgctacag	9081
Db	409	CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGACGCGAGGTATGTAGCGGTGCTACAG	468
QY	9082	agttcttgaaagtgtggcctaactacggctacactagaaggacagtatttgggtatctgcg	9141
Db	469	AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGTTGTTATCTGCG	528
QY	9142	ctctgctgaagccagttaccttcgggaaaaagagttggtagctcttgatccgcgcaaaaaa	9201
Db	529	CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCCGCAAAACAA	588
QY	9202	ccacgcgtggtagcggtgtttttttgttgtaagcagcagattacgcgcagaaaaaaag	9261
Db	589	CCACCGCTGGTAGCGGTGGTTTTTTGTGTTGCAAGCAGCAGATTACGGCGCAGAAAAAAG	648
QY	9262	gatctcaagaagatccctttgatcttttctacggggtctgacgctcagtggaacgaaaaact	9321
Db	649	GATCTCAAGAAGATCCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAAACT	708
QY	9322	cacgttaagggtatttgggtcatgagattatcaaaaaaggattctcacctagatccttttaa	9381
Db	709	CACGTTAAGGGATTTTGGTCAATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTTAA	768
QY	9382	attaaaaatgaagtttttaaatcaatcataagt	9413
Db	769	ATTAAAAATGAAGTTTAAATCAATCTAAAGT	800
RESULT 9			
BI687610			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			

BI687610 842 bp mRNA linear EST 18-SEP-2001  
603312586F1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5352717 5',  
mRNA sequence.  
BI687610  
BI687610.1 GI:15650238  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 842)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.





QY 9747 gccattgctacagggcatcgtggtgtcacgctcgtcgcttggtatggtcttcattcagctcc 9806  
Db 121 GCCATTGCTACAGGCATCGTGGTGTACGCTCGTGG-TTGGTATGGCTTCATTACAGCTCC 179  
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Db 180 GGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGC 239  
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Db 240 TCCTTCGGTCCCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCAGTGTATCACTCATGGTT 299  
QY 9927 atggcagcactgcataattctcttactgtcatgccatccgtaagatgcttttctgtgact 9986  
Db 300 ATGGCAGCACTGCATAATTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCTGTGACT 359  
QY 9987 ggtgagtactaaacaaagtcattctgtcagaatagtgatgcggcgacagtggtgctcttgc 10046  
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QY 10047 ccggcgctcaacacgggataataccgcgcacatagcagaacttttaaaagtgtcatcatt 10106  
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QY 10107 gaaaaacgttctcgggcgcaaaactctcaaggatcttaccgctgttgagatccagttcg 10166  
Db 480 GGAACACGTTCTTCGGGCGGAAAC'TCTCAAGGATCTTTACC'GCTGTGAGATCCAGTTTCG 539  
QY 10167 atgtaaccactcgtgcaccccaactgatcttcacgatcttttacttccacagcgtttct 10226  
Db 540 ATGTAACCCACTCGTGCACCCAACTGATCTTACGATCTTTTACTTTCACCAAGCGTTTCT 599  
QY 10227 gggtagcaaaaacagggaaggcaaaatccgcgcaaaagggaataaggcgacacggaaa 10286  
Db 600 GGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAA 659  
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Db 660 TGTTGAATACTCATACTCTTCCCTTTTTC'CAATATTATTGAACGCAATTATCAGCGTTAT 719  
QY 10344 tgtctcatgagcggtacacatatattgaaatgtatttagaaaaataacaaataggggttcog 10403  
Db 720 TGTCTCATGAGCGGATACATAATTGGCCTGTATTTCAGAAAATACACAATAGGGGTTCCG 779  
QY 10404 cgcacattttcccc 10416  
Db 780 -GCACATTTCCCG 791

RESULT 11  
AQ856202/c  
LOCUS  
DEFINITION nbeb0001F05f CUGI Rice BAC Library (ECORI) Oryza sativa genomic clone nbeb0001F05f, DNA sequence.  
ACCESSION AQ856202  
VERSION AQ856202.1 GI:6206659  
KEYWORDS GSS.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 757)  
AUTHORS Wing,R.A. and Dean,R.A.  
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGGG  
Class: BAC ends  
High quality sequence start: 29  
High quality sequence stop: 232.  
FEATURES  
Location/Qualifiers  
source  
1..757  
/organism="Oryza sativa"  
/strain="Japonica"  
/cultivar="Nipponbare"  
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/clone="nbeb0001F05f"  
/clone\_lib="CUGI Rice BAC Library (ECORI)"  
/tissue\_type="leaf"  
/lab\_host="E. coli DH10B"  
/note="Vector: pBACIndigo; Site\_1: EcoRI; Site\_2: EcoRI;  
Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.  
Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."  
BASE COUNT 204 a 180 c 178 g 185 t 10 others  
ORIGIN

Query Match 6.0%; Score 674.6; DB 12; Length 757;  
Best Local Similarity 98.0%; Pred. No. 1.3e-136;  
Matches 702; Conservative 0; Mismatches 12; Indels 2; Gaps 2;  
QY 8784 ggaagctccctcgtgcgtctctcctgttccgacccctgcgcgttaccggatacc-tgtccgc 8842  
Db 755 GAAAGCTCCTTCGTGCGCTCTCCTGTGTGACCCNTGCGGCTTTACGGATACNTGTNCGC 696  
QY 8843 ctctctcc-cttcgggaagcgtggcgctttctcaatgctcacgcgtgtaggtatctcagtt 8901  
Db 695 CTTTCTCCNCTTCGGAAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTT 636  
QY 8902 cggtaggtcgctcgctccaagctgggctgtgtgcacgaaccccccggttcagcccgacc 8961  
Db 635 CGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTACGCCCGACC 576  
QY 8962 gctgcgccttataccggtaactatcgcttggagtcacaccccggttaagacacgacttatcg 9021  
Db 575 GCTGCGCCTTATCCGTTAACTATCGTCTTGTAGTCCACCCGGTAAGACACGACTTATCGC 516  
QY 9022 cactggcagcagccactggtaacaggattagcagagcgaggtatgtaggcggtgctacag 9081  
Db 515 CACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAG 456  
QY 9082 agttcttgaagtgtggcctaactacggtctacactagaggacagtagtttgggtatctgcg 9141  
Db 455 ACTTCTTGAAGTGTGGCCTTAACCTACGCTACACTAGAGAACAGTATTTGGTATCTCGG 396  
QY 9142 ctctgctgaagccaggttaccttcggaaaaagagtgtgtagctcttgatccggcaacaaa 9201  
Db 395 CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAACAAA 336  
QY 9202 ccacgcgtggtagcgtgggttttttggcaagcagcagattacgcgcgcaaaaaaag 9261

Db	335	CCACCGCTGGTAGCGGTGGTGTGTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAG	276
Qy	9262	gatctcaagaagatcccttgatcttttctacggggtgtgacgctcagtggaacgaaaaact	9321
Db	275	GATCTCAAGAAGATCCTTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACT	216
Qy	9322	cacgttaagggttttggtcatgagattatcaaaaaggatcttcacctagatcccttttaa	9381
Db	215	CACGTTAAGGGATTTGGTCAAGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAA	156
Qy	9382	attaaaaatgaagtttttaaatcaatctaaagtatatatgagtaaaacttggtctgacagtt	9441
Db	155	ATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTT	96
Qy	9442	accaatgcttaatcagtgaggcaacctatctcagcgatctgtctatttcgttcaccc	9497
Db	95	ACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCTCGTTCATCC	40
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
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BASE COUNT			
ORIGIN			
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Best Local Similarity			
Matches			
Qy	9730	gtttgcgcacaagttggtgccattgctacaggcagtcgttggtgcacgctcgtcgttttgta	9789
Db	11	GTTTGGCGCAACGTTGTTGCCATFGCTACAGGCATCGTGGTGTACAGCTCGTCTTGTA	70

Qy	9790	tggcttcattcagctccggttcccaacgatcaaggcgaggttacatgatcccccatgttgt	9849
Db	71	TGGCTTCATTACAGTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGT	130
Qy	9850	gcataaaaagcgggttagctcccttcggtccctccgatcgttgtcagaagaagtggtgcccag	9909
Db	131	GCAAAAAAGCGGTAGCTCCTTCGGTCCCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCAG	190
Qy	9910	tggtatcactcatggttatggcagcactgcataaattctcttactgtcgtcgcacccgtaa	9969
Db	191	TGTTATCACTCATGTGTTATGGCAGCACTGCATAATTCTTACTGTCTCATGCCATCCGTAA	250
Qy	9970	gatgcttttctgtgactggtgagtactcaaccaaagtcattctctgagaatagtgatcgcc	10029
Db	251	GATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAAATAGTGTATCGGC	310
Qy	10030	gaccgagttgctcttgcggcggtcaacacacgggataataaccgcgcacatagcagaactt	10089
Db	311	GACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTT	370
Qy	10090	taaaagtgctcatcatctggaaaaacgttcttcggggcgaaacactctcaaggatcttaccgc	10149
Db	371	TAAAAGTGCTCATCATTTGGAAAACGTCTTCGGGGSCGAAAACTCTCAAGGATCTTACCGC	430
Qy	10150	tggtgagatccagttcgatgtaaccacactcgtgcacccaactgatcttcagcatctttta	10209
Db	431	TGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTA	490
Qy	10210	cttccaccagcgttctggtgagcaaaaaacagggaagcaaaatgcgcga--aaaaaggg	10267
Db	491	CTTTCACCAGCGTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAACAAAGGGA	550
Qy	10268	aataaggcgacacggaaaatgttgataactcactcactctctcttttccaattattgaag	10327
Db	551	ATAACGGGCGACACGGAAATGTTGAATACTCATACCTCTTCTCTTTTCAATATTATTGAAG	610
Qy	10328	catttatcagggttattgtctcatgagcgggatacatatttgaaatgattagaaaaataa	10387
Db	611	CATTATCAGGGTTATTGTCTCATGACGGGATACATATTGAATGTATTTAGAAAAATAA	670
Qy	10388	acaaatagggttcccg-cgcacatttccccgaaaaagtgccacctgacgtctaaagaaacca	10446
Db	671	ACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAAGTCCACCTAAATTGTACAGCGTTA	730
Qy	10447	ttattatcatgacatt	10462
Db	731	ATATTTCGTTAAAAATT	746
RESULT 13			
AL598527/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			



sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No s1 sequence available.  
This clone (DKF2p313O1920) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source  
Location/Qualifiers  
1. .693  
/organism="Homo sapiens"  
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/clone="DKF2p313O1920"  
/clone\_lib="313 (synonym: hlcc2)"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pTriplEx2; Site\_1: SfIIA; Site\_2: SfiIB;  
cDNA-collection"  
BASE COUNT 173 a 167 c 156 g 194 t 3 others  
ORIGIN

Query Match 6.0%; Score 669.4; DB 9; Length 693;  
Best Local Similarity 99.6%; Pred. No. 1.7e-135;  
Matches 670; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10015 aatagtgatcgggcagcgagttgctcttgcggcggtcaacacgggataataccgcgc 10074  
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Db 685 AATAGTGATCGGGCAGCGAGTTGCTCTTGCCCGCGTCAATACGGNATAATACGCGC 626  
QY 10075 cacatagcagaactttaaaagtgtctcatcattggaaaaacgttcttcggggcgaaaaactct 10134  
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Db 625 CACATAGCAGANCTTTAAAGTGCTCATCATTTGAAAACGTTCTTCGGGGCGAAAACCTCT 566  
QY 10135 caaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactgat 10194  
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Db 565 CAAGGATCTTACCGCTGTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACCTGAT 506  
QY 10195 cttcagcatctttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaatg 10254  
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Db 505 CTTCAGCATCTTTACTTTACCAAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATG 446  
QY 10255 ccgcaaaagggaataaggcgcgacacgggaaatgttgaatactcatactcttcttttc 10314  
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Db 445 CCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACATCTCTTCCTTTTC 386  
QY 10315 aatattattgaagcatttatcagggttatgtctcatgagcggatcacatatattgaatgta 10374  
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Db 385 AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTGAATGTA 326  
QY 10375 tttagaaaaataacaaatagggttccgcgcacatttcccgaaaaagtgccacctgacg 10434  
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Db 325 TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTGACG 266  
QY 10435 tctaagaaccattattatcatgacattaaactataaaaaataggcgtatcacagggccct 10494  
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Db 265 TCTAAGAAACCATTTATTATCATGACATTTAACCTATAAAAAATAGCGGTATCACAGGCGCCT 206  
QY 10495 ttcgctcgcgcgcttctcggtgatgacggtgaaaacctctgacacatgcagctcccgagga 10554  
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Db 205 TTGGTCTCGCGCGTTTTCGGTGATGACGGTGAAAACCTCTTGACACATGCAGCTCCCGGAGA 146  
QY 10555 cgggtcacagcttgctctgtaagcgggatgcggggagcagacaaagcccgtcaggcgcggtcag 10614  
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Db 145 CGGTACAGAGCTTGTCTGTAAAGCGGATGCCGGGAGCAGACAAAGCCGTCAGGGCGGTCAG 86  
QY 10615 cgggtgttgccgggtgtcggggctggcttaactatgcggcatcagagcagattgtactga 10674  
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Db 85 CGGGGTGTGGGGGTGTTCGGGGCTGGCTTAAGTATGCGGGCATCAGAGCAGATTGTACTGA 26  
QY 10675 gagtgcaccatat 10687  
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Db 25 GAGTGCACCATAT 13

RESULT 14  
AG107786/c  
LOCUS  
DEFINITION  
Pan troglodytes DNA, clone: PTB-112L09.R, genomic survey sequence.  
ACCESSION  
AG107786  
VERSION  
AG107786.1 GI:16728304  
KEYWORDS  
GSS; GSS (genome survey sequence).  
SOURCE  
Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE  
1 (sites)  
AUTHORS  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE  
BAC end sequences of Library PTB  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 723)  
AUTHORS  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama 230-0045, Japan  
(E-mail:chimpbes@psc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
COMMENT  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1. .723  
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BASE COUNT 190 a 178 c 177 g 177 t 1 others  
ORIGIN

Query Match 5.9%; Score 659.2; DB 12; Length 723;  
Best Local Similarity 99.4%; Pred. No. 2.9e-133;  
Matches 661; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8797 tgcgctctctgttccgacctgcccgttacccggataacctgtccgctttctccctcgg 8856  
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Db 722 TCGGCTCTCCTGTTCGGACCCCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGG 663  
QY 8857 gaagcgtggcgctttctcaatgctcacgctgtaggtatctcagttcaggtcgttc 8916  
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Db 662 GAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGSTATCTCAGTTCGTTAGGTCGTTTC 603  
QY 8917 gctccaagctggcgctgtgtgcagaaaccccccttcagcccgacctgccttatccg 8976  
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Db 602 GCTCCAAGCTGGGCTGTGTGCAGAAACCCNCCGTTACGCCCGACCGCTGCCTTATCCG 543  
QY 8977 gtaactatcgcttgcagtcacacccggtaagacacgacttatcgccactggcagagcca 9036  
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Db 542 GTAACATATCGTCTTGAGTCCACCCGGTAAGACACGACTTATCGCCACTGGCAGAGCCA 483  
QY 9037 ctggtaacagattagcagagcaggtatgtaggcggtgctacagagttcttgaagtgtt 9096  
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Db 482 CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGT 423  
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Db	422	GGCCTAACTACGGCTACACTAGAGAACAGTATTTGGTATCTGCGTCTGCTGAAGCCAG	363
Qy	9157	ttaccttcggaanaagagttggtagctcttgatccggcaaaacaaacccacgctggtagcg	9216
Db	362	TTACCTTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAACACCGCTGGTAGCG	303
Qy	9217	gtggtttttttgttgcaagcagcagattacgcgcagaaaaaaggatctcaagaagatc	9276
Db	302	GTGGTTTTTTTGTTCGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC	243
Qy	9277	ctttgatctttttctacggggtctgcgctcagtggaacgaaaaactcaagttaaggattt	9336
Db	242	CTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATT	183
Qy	9337	tggtcatgagattatcaaaaaaggatcttcacctagatccttttaaaattaaaaatgaagtt	9396
Db	182	TGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTT	123
Qy	9397	ttaaatcaatctaaagtatatatgagtaaaacttggtgacagttaccaatgcttaatca	9456
Db	122	TTAAATCAATCTAAAGTATATATAGATAAACTTGGTCTGACAGTTACCAATGCTTAATCA	63
Qy	9457	gtgag	9461
Db	62	GTGAG	58
RESULT 15			
LOCUS	AL645322	675 bp	mRNA linear EST 12-DEC-2001
DEFINITION	AL645322	XGC-neurula Silurana tropicalis cDNA clone	TNeu017h02 5', mRNA sequence.
ACCESSION	AL645322		
VERSION	AL645322.1	GI:16797447	
KEYWORDS	EST.		
SOURCE	western clawed frog.		
ORGANISM	Silurana tropicalis		
REFERENCE	1 (bases 1 to 675)		
AUTHORS	Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.		
TITLE	Sanger Xenopus tropicalis EST project 2001 (10_2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Huckle E Sanger Centre Hinxtan, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPICALIS_SEQUENCE_ID: TNeu017h02.sp6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.		
FEATURES	Location/Qualifiers		
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	/lab_host="Escherichia coli DH10B"		
	/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."		
BASE COUNT	153 a 185 c 174 g 163 t		
ORIGIN			

Query Match 5.9%; Score 656.2; DB 9; Length 675;  
Best Local Similarity 99.4%; Pred. No. 1.3e-132;  
Matches 669; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy	8675	ggcggtttttccataggctccgccccctgacgagcatcacaaaaatcgaagctcaagtca	8734
Db	4	GGCGTTTTTCCATA-GCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCA	62
Qy	8735	gaggtggcgaacccgacaggaactataaagataaccagggtttccccctggaagctccct	8794
Db	63	GAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGSGGTTTCCCCCTGGAAGCTCCCT	122
Qy	8795	cgtgcgctctcctgttccgacccctgcgcgttacccggataccctgtccgcctttctcccttc	8854
Db	123	CGTGGGCTCTCCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCCCTTCTCCCTTC	182
Qy	8855	gggaagcgtggcgctttctcaatgctcacgcgtgtaggtatctcagttcgggtgtaggtcgt	8914
Db	183	GGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTG	242
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 22:51:06 ; Search time 259.18 Seconds  
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Perfect score: 11206  
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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	2034.2	18.2	3875	4	US-09-039-762A-21
c 5	2034.2	18.2	3878	4	US-09-039-982A-27
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c 28	2032.6	18.1	4045	4	US-08-464-700-54	Sequence 54, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/09331581  
; Patent No. 6130070  
; GENERAL INFORMATION:  
; APPLICANT: TOHDA, Hideki  
; APPLICANT: HAMA, Yuko  
; APPLICANT: KUMAGAI, Hiromicho  
; TITLE OF INVENTION: INDUCTION PROMOTER GENE AND SECRETORY SIGNAL GENE  
; TITLE OF INVENTION: USABLE IN SCHIZOSACCHAROMYCES POMBE, EXPRESSION VECTORS  
; TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF  
; FILE REFERENCE: 0059-1142-OPCT  
; CURRENT APPLICATION NUMBER: US/09/331,581  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: PCT/JP98/04929  
; EARLIER FILING DATE: 1998-10-30  
; EARLIER APPLICATION NUMBER: JP 9-314608  
; EARLIER FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 7286  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:DNA  
US-09-331-581-3

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; Patent No. 6251627
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Sprent, Jonathan
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
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; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
; TITLE OF INVENTION: ACTIVATION OF T-CELLS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6251627th Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,641
; FILING DATE: 8-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olson, Arne M.
; REGISTRATION NUMBER: 30,203
; REFERENCE/DOCKET NUMBER: TSRI4710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-039-641-21
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Db 3123 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG 3064
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Db 3063 AGTCTTTGAAGTGGTGGCCTAACTACGGCTACACTAGAGGACAGTATTTGGPATCTGCG 3004

Qy 9142 ctctgctgaagccagttacccttcggaataagagtggttagctcttgcacgcaataaaa 9201

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Db 1443 CGCACAGATCGGTAAGGAGAAAA 1421

RESULT 4

US-09-039-762A-21/c

; Sequence 21, Application US/09039762A

; Patent No. 6255073

; GENERAL INFORMATION:

; APPLICANT: Cai, Zeling

; APPLICANT: Sprent, Jonathan

; APPLICANT: Brunmark, Anders

; APPLICANT: Jackson, Michael

; APPLICANT: Peterson, Per A.

; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS

; TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Olson & Hierl, Ltd.

; STREET: 20 No. 6255073th Wacker Drive, 36th Floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/039,762A

; FILING DATE: 16-MAR-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OLSON, Arne M.

; REGISTRATION NUMBER: 30,203

; REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 580-1180



; TELEFAX: (312) 580-1189									
; INFORMATION FOR SEQ ID NO: 21:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 3875 base pairs									
; TYPE: nucleic acid									
; STRANDEDNESS: double									
; TOPOLOGY: linear									
; MOLECULE TYPE: cDNA									
; HYPOTHETICAL: NO									
; ANTI-SENSE: NO									
US-09-039-762A-21									
Query Match									
Best Local Similarity 18.2%; Score 2034.2; DB 4; Length 3875;									
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;									
QY	8662	agttcaagaagaagcgcttttccataggtccgccccctgacgagcatcaaaaaatc	8721						
Db	3483	AGGCCGCGTGTGCTGGCGTTTTTCCATAGGCTCCGCCCTTGACGAGCATCACAAAATC	3424						
QY	8722	gacgctcaagtcagaggtggcgaaaaaccgacaggaactataaagataaccagggctttcccc	8781						
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QY	8782	ctggaagctccctcgtgcgctctcctcctgttccgaccctgcgcgttaccggataacctgtccg	8841						
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QY	8842	cctttctcccttcgggaagcggtggcgcttctcctcaatgctcaacgctgtaggtatctcagtt	8901						
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QY	9022	cactggcagcagccactggttaacaggattacgagagcgaggtatgtaggcggtgctacag	9081						
Db	3123	CACCTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGGAGGTATGTAGCGGCTGTACAG	3064						
QY	9082	agttcttgaagtgggtggcctaactacggctacactagaaggacagtatatttggtatctgcg	9141						
Db	3063	AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAGGACAGTATTGGTATCTGCG	3004						
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QY	9202	ccaccgctgtagcgggtggtttttgtttgcaagcagcagattacgcgcgagaaaaaag	9261						
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Db	2883	GATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACT	2824						
QY	9322	cacgttaagggatttttggtcatgagattatcaaaaaaggatcttccacctagatcccttttaa	9381						
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QY	9502	ttgectgactccccgtcggtagataaactacgatacggaggggttaccatcttgccccca	9561						
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QY	9622	agccagccggaaggcccgagcgcagaaagtggctctgcaactttatccgcctccatccagt	9681						
Db	2523	AGCCAGCCGGAAGGCCGAGCGCAGAGTGGTGCTCTGCAACTTTATCCGCTCCATCCAGT	2464						
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QY	10042	cttgccccggcgtcaacacgagggataataaccgcgccacatagcagaacttttaaaagtgcctca	10101						
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QY	10102	tcattggaaaaacgttcttcggggcggaacactctcaaggatcttaccgctgttgagatcca	10161						
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Db	1923	TTTCTGGGTGAGCAAAAACAGGAAGGCAAAAATGCCGCAAAAAGGGAATAAGSGCGGACAC	1864						
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RESULT 5  
US-09-039-982A-27/c  
; Sequence 27, Application US/09039982A  
; Patent No. 6225042  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zeling  
; APPLICANT: Sprent, Jonathan  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-CEL  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6225042th Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,982A  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olson, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI4710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3878 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-039-982A-27

Query Match 18.2%; Score 2034.2; DB 4; Length 3878;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 10102 tcatggaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 10161  
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Db 2046 TCATTGGAAAACGTTCTTCGGGGGGAACCTCTCAAGGATCTTACCGCTGTTGAGATCCA 1987  
  
QY 10162 gttcagtgtaacccactcgtgcaccccaactgatcttcagcatctttactttcaccagcg 10221  
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Db 1986 GTTCGATGTAACCCACTCGTGCACCCCACTGATCTTCAGCATCTTTTACTTTCACCCAGCG 1927  
  
QY 10222 tttctgggtgagcaaaaaacaggaaggcaaaaatgccgcacaaagggaataagggcgacac 10281  
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Db 1926 TTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGAATAAGGCGGACAC 1867  
  
QY 10282 ggaatgttgaatactactactcttcccttttcaatatattatgaagcatttatcagggtt 10341  
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Db 1866 GGAATGTTGAATACTCATACTCTTCCCTTTTCAATATTATTTGAAGCATTTATCAGGGTT 1807  
  
QY 10342 attgtctcatgagcgggatacatatttgaatgtatttagaaaaataaacaataggggttc 10401  
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Db 1806 ATTGTCTCATGAGCGGATACATATTGTAATGTATTTAGAAAAATAAACAAATAGGGGTT 1747  
  
QY 10402 cgcgcacatttccccgaaaaagtgccacctgcacgtctctaagaaacattattatcatgacat 10461  
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Db 1746 CGCGCACATTTCGCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTTATTATCATGACAT 1687  
  
QY 10462 taacctataaaaaataggcgtatcacgagggcccttctcgtcgcgcttctcgtgatgacg 10521  
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Db 1686 TAACCTATAAAAAATAGCGGTATCACGAGGGCCCTTTCGTCTCGCGCGTTTCGGGTGATGACG 1627  
  
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QY 10582 ccgggagcagacaaagcccgctcagggcgcgctcagcgggtgttgcggggtgcggcgctggc 10641  
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QY 10642 ttaactatgcggcatcagagcagattgtactgagagtgaccatatgcgggtgtgaaatac 10701  
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Db 1506 TTAACATATGCGGCATCAGACAGAGATTGTACTGAGAGTGCACCATATGCGGGTGTGAAATAC 1447  
  
QY 10702 cgcaccgaatcgcgcggaactaa 10724  
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Db 1446 CGCACAGATCGGTAAGGAGAAAA 1424

RESULT 6  
US-09-641-27/c  
; Sequence 27, Application US/09039641  
; Patent No. 6251627  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zeling  
; APPLICANT: Sprunt, Jonathan  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.

; STREET: 20 No. 6251627th Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,641  
; FILING DATE: 8-MAR-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olson, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI4710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3878 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-09-039-641-27

Query Match 18.2%; Score 2034.2; DB 4; Length 3878;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 8662 agttcaagaagaagcggttttccataggtccgcggccccctgacgagcatcacaaaaatc 8721  
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Db 3486 AGCCGCGCTTGCTGGCGTTTTCATAGGCTCGGCCCTCGCCCTGACGAGCATCACAAAATC 3427  
  
QY 8722 gacgctcaagtcaagtggtggcgaacccgacaggactataaaagataccaggcgttcccc 8781  
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Db 3426 GACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACAGCGCTTCCCC 3367  
  
QY 8782 ctggaagctccctcgtgcgtctcctgttccgacccctgccgcttaccggatacctgctcg 8841  
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Db 3366 CTGGAAGCTCCCTCGTGCCTCTCCTGTTCGACCCCTGCCGCTACCGGATACCTGTCCG 3307  
  
QY 8842 cctttctcccttcgggaagcgtggcgcttctcaatgctcaogctgtaggtatctcagtt 8901  
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Db 3306 CCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTT 3247  
  
QY 8902 cgggtgtaggtcgttcgctccaagctgggctgtgtgacgaaccccccttcagcccgacc 8961  
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Db 3246 CGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCTTCAGCCCGACC 3187  
  
QY 8962 gctgcgcttatccgggtaactatcgtctttagtccaaaccccgtaagacacgacttatcgc 9021  
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Db 3186 GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCCGTAAGACACGACTATCGC 3127  
  
QY 9022 cactggcagcagccactggttaacaggatttagcagagcgaggtatgtaggcgtgtacag 9081  
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Db 3126 CACTGGCAGCAGCCACTGGTAACAGGATTACAGAGCGGAGGTATGTAGCGGTGTACAG 3067  
  
QY 9082 agttctgaagtggtggccctaactacggtacactagaagacagatatttgggtatctgcg 9141  
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Db 3066 AGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAGGACAGTATTGGTATCTCGG 3007  
  
QY 9142 ctctgctgaagccagttacccttcggaaaaaagagttggtagctcttgatccgggcaaaaaa 9201  
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Db 3006 CTCTGCTGAAGCCAGTTACTCTCGGAAAAAGAGTTGGTAGCTTGTATCCGGCAACAAA 2947





; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-039-762A-27

Query Match 18.2%; Score 2034.2; DB 4; Length 3878;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY	8662	agttcaagaagaaggcgtttttccataggtccgcggccctccgcggccctgacgagcatcacaaaaatc	8721
Db	3486	AGGCCGCGTGTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC	3427
QY	8722	gacgctcaagtcagaggtgcgaaacccgacaggactataaagataccaggcgtttccccc	8781
Db	3426	GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCCAGGCGTTTCCCC	3367
QY	8782	ctggaagctccctcgtgcgtctctcgtgttccgacccctgcggttacccggataccctgtccg	8841
Db	3366	CTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCG	3307
QY	8842	cctttctcccttcgggaagcgtggcgctttctcaatgctcacgctgtaggtatctcagtt	8901
Db	3306	CCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTT	3247
QY	8902	cgggtgaggtcgttcgctccaaagctggcgctgtgtgcacgaaccccccggttcagcccgacc	8961
Db	3246	CGGTGTAGTCTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACC	3187
QY	8962	gctgcgcttatcccggtaaactatcgtctctgagtcocaaacccggtaagacacgacttatcgc	9021
Db	3186	GCTGGCGCTTATCCGGTAACHTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC	3127
QY	9022	cactgcagcagccactggttaacaggattagcagagcgaggtatgtagcggtgctacag	9081
Db	3126	CAC TGGCAGCAGCCACTGGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAG	3067
QY	9082	agttctgaagtggtggcctaactacggtacacggtacagagacagtatttggtatctgcg	9141
Db	3066	AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCG	3007
QY	9142	ctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccgcgcaaacaaa	9201
Db	3006	CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGTGTAGCTCTTGATCCGSCAACAAA	2947
QY	9202	ccacgcgtggtagcgggtgtttttgtttgcaagcagcagattacgcgcagagaaaaaag	9261
Db	2946	CCACCGCTGGTAGCGGTGGTTTGTGTTGCAAGCAGCAGATTACGGCGCAGAAAAAAG	2887
QY	9262	gatctcaagaagatcctttgatcttttctacggggtctgacgctcagtcagtcgaacgaaaaact	9321
Db	2886	GATCTCAAGAAGATCCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGGAACGAAAAC	2827
QY	9322	cacgttaagggttttgggtcatgagattatacaaaaggatcttccacctagatoccttttaa	9381
Db	2826	CACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAA	2767
QY	9382	attaaaaatgaagtttttaaatcaatctaaagtatatatgagtaaaccttggtctgacagtt	9441
Db	2766	ATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACCTTGGTCTGACAGTT	2707
QY	9442	accaatgcttaatcagtgagccactatctcagcgatctgtctatttcttcctcatccatag	9501
Db	2706	ACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCTGTCATCCATAG	2647
QY	9502	ttgcctgactccccctggtgtagataaactacgatacgggagggccttaccatctggcccca	9561
Db	2646	TTGCCTGACTCCCCGCTGCTGATGATAACTACGATACGGGAGGCTTACCATCTGGCCCCA	2587
QY	9562	gtgctgcaatgataccgcgagacccacgctcaccggtccagatttatcagcaataaac	9621

Db	2586	GTGCTGCAATGATACCGCGAGACCCACGCTCACGGGCTCCAGATTTATCAGCAATAAAC	2527
QY	9622	agccagccggaaggccgagcgcagaagtgttcctgcaactttatccgcctccatccagt	9681
Db	2526	AGCCAGCCGGAAGSGCGAGCGCAGAAGTGSTCTCTGCAACTTTATCCGCCTCCATCCAGT	2467
QY	9682	ctattaattgttcgcggaagcctagagtaagtagttcgcagtttaagtttgcgcaacg	9741
Db	2466	CTATTAAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGC	2407
QY	9742	ttgttgccattgctacaggcacgtcgtggtgtcagcgtcgtcgtttggtatggcttcattca	9801
Db	2406	TTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATTCA	2347
QY	9802	gctccggttcccacgatcaaggcgagttacatgatcccccatgttgtgcaaaaaagcgg	9861
Db	2346	GCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG	2287
QY	9862	ttagctccttcggtcctccgatcgttgtcagaagtaagttggcgcgagtggttatcactca	9921
Db	2286	TTAGCTCCTTCGSTCCTCCGATCGTGTGTAGAAAGTAAGTTGGCCGACGTGTATCACTCA	2227
QY	9922	tggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgcttttctg	9981
Db	2226	TGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCTG	2167
QY	9982	tgactggtgagtactcaaccaagtcattcttactgtcatgccatccgtaagatgcttttctg	10041
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QY	10042	cttgccccggcgtcaacacagggataataaccgcgcacatagcagaacctttaaaagtgtca	10101
Db	2106	CTTGCCCCGGCGTCAATACGGGATAATACCGCGGCCACATAGCAGAACTTTAAAAAGTGCTCA	2047
QY	10102	tcattggaaaaagttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca	10161
Db	2046	TCATTGGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCA	1987
QY	10162	gttcgatgtaacccactcgtgcacccaactgatcttcagcatcttttactttcacccagcg	10221
Db	1986	GTTTCGATGTAACCCCACTCGTGTGCACCCAACATGATCTTCAGCATCTTTTACTTTTCA	1927
QY	10222	tttctgggtgagcaaaaaaggaaggcaaaaatgccgcgcaaaaaaggaaataagggcgacac	10281
Db	1926	TTTCTGGGTGAGCAAAAACAGGAAGSAAAAATGCCGCAAAAAGGGAATAAGGGCGACAC	1867
QY	10282	gaaaatgttgaatactcatactcttcccttttccaataattattgaagcatttatcagggtt	10341
Db	1866	GGAAATGTTGAATACTCATACTCTCTCTCTTTTCAATAATTTATGAAGCATTTTATCAG	1807
QY	10342	attgtctcatgagcgggatacatatttgaaatgtatttagaaaaataaacaataaggggttc	10401
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Db	1686	TAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCCTCGCGCGTTTCGGTGATG	1627
QY	10522	gtgaaaacctctgacacatgcagctccccggagacggtcacagcttgcgtgtaagcggatg	10581
Db	1626	GTGAAAAACCTCTGACACATGCAGCTCCCGAGACGGTCACAGCTTGCTGTGAAGCGGATG	1567
QY	10582	ccggagcagacaaagcccgtcagggcgcgctcagcgggtgttggtggcggtgtcgggctggc	10641
Db	1566	CCGGAGCAGACAAGCCCCGTAGGGCGCGTACGCGGTGTGGCGGGTGTTCGGGCTGGC	1507
QY	10642	ttaactatgcggcatcagagcagattgtactgagagtgcaccatatatgcggtgtgaaatac	10701
Db	1506	TTAAC TATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATAC	1447







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QY 9922 tggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgcttttctg 9981

Db 2231 TGGTTATGGCAGCACTGCATAATCTCTTACTGTGATGCCATCCGTAAGATGCTTTTCTG 2172

QY 9982 tgactggtgagtactcaaccaagtcattctcattctgtgataagtagtgcgagaccgagttgct 10041

Db 2171 TGACTGGTGAGTACTCAACCAAGTCATTCTTGAGATAAGTGTATGCCGCGACCGAGTTGCT 2112

QY 10042 cttgccccggtcacaacaggggataataaccgccccacatagcagaactttaaagtgtca 10101

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Db 2051 TCATTGGAACAGTCTCTCGGGCGAAAACTCTCAAGGATCTTACCGTGTGTGAGATCCA 1992

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Db 1991 GTTCGATGTAACCCACTCGTGCACCCCAACTGATCTCAGCATCTTTTACTTTCAACGCG 1932

QY 10222 tttctgggtgagcaaaaaacaggaaggcaaaaatgccgcaaaaaagggaataaggcgacac 10281

Db 1931 TTTCTGGTGAGCAAAAACAGGAAGGCAAAAATGCCGAAAAAAGGAATAAGGGCGACAC 1872

QY 10282 gaaaatgtgaatactcatactcttctcttcaatattattgaagcatttatcagggtt 10341

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QY 10342 attgtctcatgagcggatacatatttgaatgtatttagaaaaataaacaataaggggttc 10401

Db 1811 ATTGCTCTCAGCGGATACATATATTGAATGTATTTAGAAAAATAAACAAATAGGGGTTTC 1752

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Db 1451 CGCACAGATCGGTAAGGAGAAAA 1429

RESULT 10

US-09-039-762A-30/c

; Sequence 30, Application US/09039762A

; Patent No. 6255073

; GENERAL INFORMATION:

; APPLICANT: Cai, Zeling

; APPLICANT: Sprent, Jonathan

; APPLICANT: Brunmark, Anders

; APPLICANT: Jackson, Michael

; APPLICANT: Peterson, Per A.

; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS

; TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Olson & Hierl, Ltd.

; STREET: 20 No. 6255073th Wacker Drive, 36th Floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/039,762A

; FILING DATE: 16-MAR-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OLSON, Arne M.

; REGISTRATION NUMBER: 30,203

; REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 580-1180

; TELEFAX: (312) 580-1189

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3883 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-09-039-762A-30

Query Match 18.2%; Score 2034.2; DB 4; Length 3883; Best Local Similarity 99.1%; Pred. NO. 0; Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;									
Qy	8662	agttcaagaagaagcgctttttccataggtccgccccctgacgagcatcacaaaaac	8721						
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Qy	8722	gacgctcaagtcagaggtggcgaaccccgacagactataaagataccaggcgctttcccc	8781						
Db	3431	GACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAAGCGTTTCCCC	3372						
Qy	8782	ctggaagctccctcgtcgctctcctgttcccgacctgcccgttacccgataccctgtccg	8841						
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Qy	8842	cctttctcccttcgggaagcgtggcgcttttctcaatgctcacgcgtgtaggtatctcagtt	8901						
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Qy	8902	cggtgtaggtcgttcgctccaagctgggctgtgtgcacgaaccccccggttcagccgacc	8961						
Db	3251	CGGTGTAGTTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGACC	3192						
Qy	8962	gctgcgccttatccggtaactatcgtctgttagtccaaacccggtaagacacgacttatcgc	9021						
Db	3191	GCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAACCCCGTAAGACACGACTTATCGC	3132						
Qy	9022	cactggcagcagccactggttaacaggattagcagagcgaggtatgtaggcggtgctacag	9081						
Db	3131	CAC TGGCAGCAGCCACTGTGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAG	3072						
Qy	9082	agttctgaagtggtggccctaactacggctacactagaaaggacagtatttggtatctgcg	9141						
Db	3071	AGTTCTTGAAGTGGTGGCCTAAC TACGGCTACACTAGAAGGACAGTATTTGGTATCTGCG	3012						
Qy	9142	ctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatcccgcaacaaa	9201						
Db	3011	CTCTGCTGAAGCCAGTTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAA	2952						
Qy	9202	ccaccgctggtagcggtggtttttgtttgcaagcagcagattacgcgcagaaaaaaag	9261						
Db	2951	CCACCGCTGGTAGCGGTGGTTTTTTTGTGTCGAAGCAGCAGATTACGCGCAGAAAAAAG	2892						
Qy	9262	gatctcaagaagatcccttgatctttctacgggggtctgacgctcagtggaacgaaaaact	9321						
Db	2891	GATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGTCTTGACGGTCTAGTGGAAACGAAACT	2832						
Qy	9322	cacgttaagggattttggtcoatgagattatacaaaaaggatcttcaoctagatccctttaa	9381						
Db	2831	CACGTTAAGGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCCTTTAA	2772						
Qy	9382	attaaaaatgaagtttttaaatcaatctaaaagtatatatgagtaaaacttggctcgacagtt	9441						
Db	2771	ATTA AAAATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTT	2712						
Qy	9442	accaatgcttaatcagtgaggcacctatctcagcgatctgtctatttctgttcatccatag	9501						
Db	2711	ACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGGATCTGTCTATTTCTGTTTCATCCATAG	2652						
Qy	9502	ttgcctgaactccccctgctgtagataaactacgatacgggagggcttaccatctggccccca	9561						
Db	2651	TTGCCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCCA	2592						
Qy	9562	gtgctgcaatgataccgcgagagacccacgctcacgggtccagatttatcagcaataaaacc	9621						
Db	2591	GTGCTGCAATGATACCGCGAGACCCACCGCTCACCGGCTCCAGATTTATCAGCAATAAAACC	2532						
Qy	9622	agccagccggaagggccgagcgagaaagtgtcctgtcaactttatccgcctccatccagtt	9681						
Db	2531	AGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGCAACTTTATCCGCCCTCCATCCAGT	2472						

Qy	9682	ctattaattgttgcggggaagctagagtaagtagttcgcagtgtaataagtttgcgcaacg	9741						
Db	2471	CTATTAAATTGTTGCCGGAAGCTAGAGTAAGTAGTTGCCCAGTTAATAGTTTGGCAACG	2412						
Qy	9742	ttgttgccattgctacaggcatcgtgtgtlcaacgctcgtgtgttggtatgggttcattca	9801						
Db	2411	TTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTCGTCTGGTATGGCTTCATTCA	2352						
Qy	9802	gctccgggttcccaacgatcaaggcgaggttacatgatcccccatgttgtgcaaaaaagcgg	9861						
Db	2351	GCTCCGGTTCCCAACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG	2292						
Qy	9862	ttagctccttcggctcccgatcgttgtcaagaagtaagtgtggccgagtggttatcaactca	9921						
Db	2291	TTAGCTCCTTCCGTCCTCCGATCGTTGTCAAGTAAGTTGGCCGCAGTGTGTATCACTCA	2232						
Qy	9922	tggttatggcagcactgcataaattctcttactgtcatgccatccgtaagatgctttttctg	9981						
Db	2231	TGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATGCCATCCGTAAAGTGTCTTCTG	2172						
Qy	9982	tgaactggtgagtactcaaccaagtcattctcttactgtcatgccatccgtaagatgcttttctg	10041						
Db	2171	TGACTGTTGAGTACTCAACCAAGTCATCTCTGAGAATAGTGTATGCGGGACCGAGTTGCT	2112						
Qy	10042	cttgcggcggtcaacacgggataaataccgcgcccacatagcagaaacttttaaagtgctca	10101						
Db	2111	CTTGCCCCGGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGTGTCTCA	2052						
Qy	10102	tcaattggaaaaacgtttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca	10161						
Db	2051	TCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCA	1992						
Qy	10162	gttcgatgtaaccactcgtgcaccactgatcttctcagcatcttttactttcaccagcg	10221						
Db	1991	GTTCGATGTAACCCACTCGTGCACCCCAACTGATCTTCAAGCATCTTTTACTTTCACCAGCG	1932						
Qy	10222	ttctcgtggtgagcaaaaaacaggaaggcaaaatgccgcacaaaaagggaataagggcgacac	10281						
Db	1931	TTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACAC	1872						
Qy	10282	ggaaatgttgaaatactcatctcttctccttttttcaatatattgaagcaatttatcaggggtt	10341						
Db	1871	GGAAATGTTGAATACTCATACTCTTCTCTTTTCAATATTATTGAAGCATTTATCAGGGTT	1812						
Qy	10342	attgtctcatgagcgggatacatatttgaatgtatttagaaaaataaacaataaggggttc	10401						
Db	1811	ATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTT	1752						
Qy	10402	cgcgcacatttccccgaaaaagtgccacctgacgtctaaagaaaccatttatcatgatgat	10461						
Db	1751	CGCGCACATTTCCCCGAAAAGTGCCACCTGACGCTCTAAGAAACCATTTATTATCATGACAT	1692						
Qy	10462	taacctataaaaaataggcgtatcacgagggcccttctcgtctcgcgcgtttcgggtgatgacg	10521						
Db	1691	TAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCTCGTCTCGCGCGTTTCGGTGTATGACG	1632						
Qy	10522	gtgaaaaacctctgacacatgcagctccccggagacgggtcacagcttgtctgaagcggatg	10581						
Db	1631	GTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCAAGCTTGTCTGTAAAGCGGATG	1572						
Qy	10582	ccgggagcagacaagcccgtcagggcgcgctcagcggtgtgtggcggggtgtcggggtggc	10641						
Db	1571	CCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAAGGGGTGTGGCGGGGTGTCCGGGGCTGGC	1512						
Qy	10642	ttaactatgcggcatcagagcagatgttactgtactgtgagagtccaccatatgcggtgtgaaatac	10701						
Db	1511	TTAACTATGCGGCATCAGAGCAGATTGTACTGTAGAGTGCACCATATGCGGGTGTGAAATAC	1452						
Qy	10702	cgcacccaatcgcgcggaaactaa	10724						
Db	1451	CGCACAGATGCGTAAGGAGAAAA	1429						



RESULT 11  
US-09-039-982A-24/c  
; Sequence 24, Application US/09039982A  
; Patent No. 6225042  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zeling  
; APPLICANT: Sprent, Jonathan  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-CEL  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6225042th Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,982A  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olson, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI4710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3908 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEtical: NO  
; ANTI-SENSE: NO  
US-09-039-982A-24

Query Match 18.2%; Score 2034.2; DB 4; Length 3908;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY	8662	agttcaagaagaaggcggtttttcccataggtccgccccctgacgagcatcacaaaaatc	8721
Db	3516	AGCGCGGTGCTGGCGTCTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATC	3457
QY	8722	gacgctcaagtcagagggtggcgaaacccgacaggactataaagataccaggcggtttcccc	8781
Db	3456	GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCC	3397
QY	8782	ctggaaagctccctcgtgcgtctctcgtttccgaccctgcgcttaaccggataacctgtccg	8841
Db	3396	CTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCG	3337
QY	8842	cctttctcccttcgggaaagcgtggcgcttttctcaatgctcagcgtgtaggtatctcagtt	8901
Db	3336	CCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACCGTGTAGGTATCTCAGTT	3277
QY	8902	cgggtgtaggtcgttcgctccaagcgtggcgcttttctcaatgctcagcgtgtaggtatctcagtt	8961
Db	3276	CGGTGTAGTGTGCTCGCTCCAAAGCTGGGCTGTGTGCACGAAACCCCGGTTTCAGCCGACC	3217
QY	8962	gctgcgccttatcccggttaactatcgtctttagtccaaaccccggttaagacacgacttatcgc	9021

Db	3216	GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC	3157
QY	9022	cactggcagcagccactggtaaacaggattagcagagcgaggtatgtagcggtgctacag	9081
Db	3156	CAC TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAG	3097
QY	9082	agttcttgaagtggtggccctaactacggctacactagaagacagtatatttgggtatctgcg	9141
Db	3096	AGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTCGG	3037
QY	9142	ctctgctgaagccagttaccttcggaaaaaagattggtagctcttgatcccgcaaaaaaa	9201
Db	3036	CTCTGCTGAAGCCAGTTACCTTCGGAAAAAAGACTGGTAGCTCTTGATCCGGCAACAAA	2977
QY	9202	ccaccgctggtagcgggtgtttttttgttttgcaagcagcagattacgcgcagaaaaaaag	9261
Db	2976	CCACCGCTGCTAGCGGTGGTGTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAG	2917
QY	9262	gatctcaagaagatcccttttgatctttctacgggggtctgacgctcagtggaacgaaaaact	9321
Db	2916	GATCTCAAGAAGATCCTTTTGATCTTTCTACGGGTCTGACGCTCAGTGAACGAAAAACT	2857
QY	9322	cacgttaagggtatttgggtcatgagattatcaaaaaggatcttcacccatagatccctttaa	9381
Db	2856	CACGTTAAGGGATTTTGGTCAATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTAA	2797
QY	9382	attaaaaatgaagtttttaaatcaatctaagttatataatagtaaaacttggctgacagtt	9441
Db	2796	ATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATAGTAAACTTGGTCTGACAGTT	2737
QY	9442	accaatgcttaatcagtgaggcacctatctcagggatctgtctatttcgttccatccatag	9501
Db	2736	ACCAATGCTAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCGTTTCATCCATAG	2677
QY	9502	ttgcctgactccccgctcgtgtagataactacgatacgggagggcttaccatctggcccca	9561
Db	2676	TTGCCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCA	2617
QY	9562	gtgctgcaatgatataccgcgagacccacgctcacgggtctccagattttatcagcaataaacc	9621
Db	2616	GTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTATCAGCAATAAAC	2557
QY	9622	agccagccggaaggccgagcgcagaagtggtctctgcaactttatccgctccatccagt	9681
Db	2556	AGCCAGCCGGAAGGCGGAGCGCAGAGTGGTCTCTGCTCAACTTTATCCGCTCCATCCAGT	2497
QY	9682	ctattaattgttgccgggaagctagagtaagtagtgcgccaagttaatagtttgcgcaacg	9741
Db	2496	CTATTAAATGTTGCCGGGAAGCTAGAGTAAGTAGTGCAGTTAATAGTTTGGCGCAAG	2437
QY	9742	ttgttgccattgctacaggcatcgtggtgtcagcgtcgtcgtttgtgtatggcttcattca	9801
Db	2436	TTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTCTGTTTGGTATGGCTTCATTCA	2377
QY	9802	gctccggttcccaacgatcaaggcaggttacatgatcccccatgttgtgcaaaaaagcgg	9861
Db	2376	GCTCCGGTTCCAAACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG	2317
QY	9862	ttagctccttcggtcctccgatcgttgtcagaagtaagtggccgcagttgttatcactca	9921
Db	2316	TTAGCTCCTTCGGTCTCCGATCGTGTTCAGAAAGTAAAGTTGGCCGAGTGTATCACATCA	2257
QY	9922	tgggtatggcagcactgcataattcttactgtccatgccatccgtaagatgctttcttg	9981
Db	2256	TGGTTATGGCAGCACTGCATAATTCTTACTGTATGCCATCCGTAAGATGCTTTTCTGT	2197
QY	9982	tgactggtgagtgactcaaccaggtcattcttgagaatagttgatgcggcgaccgagttgct	10041
Db	2196	TGACTGGTGTAGTACTCAACCAAGTCATCTTGAGATAGTGTATGCGCGACCGAGTTGCT	2137
QY	10042	cttgccccggtgcaacacgggataataaccgcgcacatagcagaaactttaaaagtgtca	10101
Db	2136	CTTGCCCCGGCTCAATACGGGATAATAACCGCCACACATAGCAGAACTTAAAAAGTGCTCA	2077

QY 10102 tcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgagatcca 10161  
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Db 2076 TCATGGAACAGTTCTTCGGGGCGAAACTCTCAAGGATCTTACCGCTGTGAGATCCA 2017  
  
QY 10162 gttcagtgtaaccactcgtgcaccccaactgatcttcagcatcttttaactttcaccagcg 10221  
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Db 2016 GTTCGATGTAACCCACTCGTGCACCCCACTGATCTTCAGGATCTTTTACTTTCACCAGCG 1957  
  
QY 10222 tttctggggtgagcaaaaacaggaagcgcaaaaatgccgcaaaaaagggaataagggcgacac 10281  
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Db 1956 TTTCTGGGTGAGCAAAACAGGAAGGCGCAAAATGCCGCAAAAAGGGAATAAGGGCGACAC 1897  
  
QY 10282 ggaatggtgaatactcatcactctctctcttttcaatatattgaagcatttatcagggtt 10341  
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Db 1896 GGAATGTTGAATACTCATACTCTCTCCTTTTCAATATTATTGAAGCATTTATCAGGGTT 1837  
  
QY 10342 attgtctcatgagcgggatacatatttgaatgtatttagaaaaataaacaataaggggttc 10401  
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Db 1836 ATTGCTCATGAGCGGATACATATTGTAATGTATTTAGAAAAATAACAATAAGGGGTTT 1777  
  
QY 10402 cgcgcacatttccccgaaaaagtgccacctgacgtctcaagaaaccatttatcatgacat 10461  
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Db 1776 CGCGCACATTTCCCGAAAAAGTGCCACCTGACGTCTAAGAAACCATTTATTATCATGACAT 1717  
  
QY 10462 taacctataaaaataggcgtatcacgagggcccttctcgtctcgcgcgttttcggtgatgacg 10521  
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Db 1716 TAACCTATAAAAATAGGCGGTATCACGAGGCCCTTTTCGTCTCGCGCGTTTCGCTGATGACG 1657  
  
QY 10522 gtgaaaacctctgacacatgcagctcccgagacgggtcacagcttgtctgtaagcggatg 10581  
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Db 1656 GTGAAACCTCTGACACATGCAGCTCCGGGAGACGGTCACAGCTTGTCTGTAAGCGGATG 1597  
  
QY 10582 cgggagcagacaaagcccgctcagggcgcggtcagcgggtgttgcggggtgcggtggc 10641  
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Db 1596 CCGGAGCAGACAAAGCCGTCAGGGCGGCTCAGCGGCTGTTGGCGGCTGCGGGGCTGGC 1537  
  
QY 10642 ttaactatgcggcatcagagcagattgtactgagagtgcaccatatcggtgtgaaatac 10701  
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Db 1536 TTAACATATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGGTGTGAAATAC 1477  
  
QY 10702 cgcaccgaatcgcgcggaaactaa 10724  
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Db 1476 CGCACAGATCGGTAGGAGAAAA 1454

RESULT 12  
US-09-039-641-24/c  
; Sequence 24, Application US/09039641  
; Patent No. 6251627  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zeling  
; APPLICANT: Sprent, Jonathan  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR  
; ACTIVATION OF T-CELLS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6251627th Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,641

; FILING DATE: 8-MAR-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olson, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI4710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3908 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-039-641-24

Query Match 18.2%; Score 2034.2; DB 4; Length 3908;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
  
QY 8662 agttcaagaagaagcggtttttccataggtccgccccctgacgagcatacaaaaaatc 8721  
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Db 3516 AGGCCGCGTGTGCTGGCGTTTTCATAGGCTCCGCCCTCGACGAGCATCACAAAATC 3457  
  
QY 8722 gacgtcaagtcagaggtggcgaaccgcagacagactataaagataccagggtttcccc 8781  
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Db 3456 GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC 3397  
  
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QY 8842 cttttcccttcgggaagcgtggcgctttctcaatgctcacgctgtaggtatctcagtt 8901  
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QY 8962 gctgcgccttatccggttaactatcgtcttgagtcctcaaccccggttaagacacgactatcgc 9021  
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QY 9082 agttcttgaagtgtggcctaactacggtctacactagaaggacagtatatttggtatctgcg 9141  
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Db 3096 AGTTCTTGAAGTGGTGGCCTAACTACGCGTACACTAGAGGACAGTATTTGGTATCTCGC 3037  
  
QY 9142 ctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatcccgcaaaaaa 9201  
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QY 9202 ccaccgctggtagcgtgggtttttttgttttgcaagcagcagattacgcgcagaaaaaag 9261  
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Db 2976 CCACCGCTGGTAGCGGTGGTTTTTTTGTGTGCAAGCAGCAGATTACGCGCAGAAAAAAG 2917  
  
QY 9262 gatctcaagaagatcctttgatctttttctacgggggtcgtgacgctcagtggaacgaaaact 9321  
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QY 9322 cacttaagggaatttttggtcatgagattatcaaaaaaggatcttcacctagatccttttaa 9381  
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Db 2856 CACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTTCACCTAGATCCTTTTAA 2797

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Db 2796 ATTAAAAATGAAGTTTAAATCAATCAAAAGTATATATGAGTAAACTTGGTCTGACAGTT 2737  
QY 9442 accaatgcttaataoagtgaggcaacctatctcagcgatctgtctatttcgttccatccatag 9501  
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Db 2736 ACCAATGCTTAATCAGTGAGGCAACCTATCTCAGCGATCTGTCTATTTCGTTCAATCCATAG 2677  
QY 9502 ttgcctgactccccgtcgtgtagataaactacgactcaccggtccagatttatcagcaataaaacc 9561  
|||||  
Db 2676 TTGCCTGACTCCCGCTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCA 2617  
QY 9562 gtgctgcaatgataccgcgagacccacgctcaccggtccaggtccagatttatcagcaataaaacc 9621  
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Db 2616 GTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTATCAGCAATAAAACC 2557  
QY 9622 agccagccggaaggccgagcgagaaagtggctcctgcaactttatccgcctccatccagt 9681  
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Db 2556 AGCCAGCCGGAAGGCCGAGCGCAGAGTGGTCTCTGCAACTTTATCCGCCCTCCATCCAGT 2497  
QY 9682 ctattaattgttcgcggaagctagagtaagtagttcgcaggttaataagtttgcgcaacg 9741  
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Db 2496 CTATTAAATTGTTGCCGGAAGCTAGAGTAACTAGTTGCCAGTTTAAATAGTTTGCGCAACG 2437  
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Db 2436 TTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTCTGTTTGGTATGGCTTCATTCA 2377  
QY 9802 gctccggttcccaacgatcaaggcgagttacatgatcccccatggttgccgcagtggttatcaactca 9861  
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Db 2376 GCTCCGGTTCCCAACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAAGCGG 2317  
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Db 2316 TTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCAGTGTATCACTCA 2257  
QY 9922 tggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgcttttctg 9981  
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Db 2256 TGGTTATGGCAGCACTGCATAATTCTCTTACTGTCAATCCGTAAAGATGCTTTTCTG 2197  
QY 9982 tgactggtgagtactcaaccaagtcatctcgagaatagtgtagtcggcgaccgagttgct 10041  
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Db 2196 TGACTGGTGAGTACTCAACCAAGTCATTCTGAGAAATAGTGATGCGGCGACCGAGTTGCT 2137  
QY 10042 cttgcccggcgtcaacacgggataataaccgcgccacatagcagaactttaaaagtgtca 10101  
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Db 2136 CTTGCCCGGCGTCAATACGGGATAATACCCGCCCCACATAGCAGAACTTTAAAAAGTCTCA 2077  
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US-09-039-762A-24/c  
; Sequence 24, Application US/09039762A  
; Patent No. 6255073  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Zeling  
; APPLICANT: Sprent, Jonathan  
; APPLICANT: Brunmark, Anders  
; APPLICANT: Jackson, Michael  
; APPLICANT: Peterson, Per A.  
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,762A  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OLSON, Arne M.  
; REGISTRATION NUMBER: 30,203  
; REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 580-1180  
; TELEFAX: (312) 580-1189  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3908 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-039-762A-24

Query Match 18.2%; Score 2034.2; DB 4; Length 3908;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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RESULT 14  
US-09-194-285-7/c  
; Sequence 7, Application US/09194285  
; Patent No. 6355479  
; GENERAL INFORMATION:  
; APPLICANT: Webb, Susan R.

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; APPLICANT: Winqvist, Ola
; APPLICANT: Karlsson, Lars
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: MHC Class II Antigen Presenting Systems
; FILE REFERENCE: TSRI 536.1
; CURRENT APPLICATION NUMBER: US/09/194,285
; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: PCT/US97/08697
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 60/018,175
; PRIOR FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4713
; TYPE: DNA
; ORGANISM: Mus musculus
us-09-194-285-7

Query Match      18.2%; Score 2034.2; DB 4; Length 4713;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
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20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	11206	100.0 11206 21	AAZ47807 Vector for trapping
2	2628.4	23.5 2646 15	AAQ61607 Mutated GAL4 gene
c 3	2439.6	21.8 7869 23	ABL05134 Drosophila melanog
4	2102.8	18.8 7286 20	AAZ57224 WO 9923223 Seq ID
c 5	2034.2	18.2 3753 24	ABA04129 Plasmid pHCE19T(II
c 6	2034.2	18.2 3755 24	ABA04130 Plasmid pHCE19(II)
c 7	2034.2	18.2 4713 19	AAV12067 Murine IAd alpha c
c 8	2034.2	18.2 4724 19	AAV12068 Murine IAd beta ch
9	2034.2	18.2 4776 20	AAZ77617 Expression constru

10	2034.2	18.2	4776	20	AAZ77614	Expression constru
11	2034.2	18.2	5323	17	AAT13390	Hybrid vector pSF1
12	2034.2	18.2	5364	17	AAT13393	Hybrid vector pMW1
13	2034.2	18.2	5374	21	AAC60706	Primers attached v
14	2034.2	18.2	5421	21	AAC68299	SV40/APPA plasmid
15	2034.2	18.2	5462	21	AAC60707	Primers attached v
16	2034.2	18.2	5465	20	AAZ20088	Plasmid pUBIAC. C
17	2034.2	18.2	5639	20	AAZ57972	Recombinant DNA ve
c 18	2034.2	18.2	5897	20	AAV63741	Plasmid pTGP190-1
c 19	2034.2	18.2	5932	21	AAZ45928	Nucleotide sequenc
c 20	2034.2	18.2	6116	21	AAC68297	R15/APPA plasmid c
c 21	2034.2	18.2	6142	21	AAZ45932	Nucleotide sequenc
c 22	2034.2	18.2	6142	21	AAZ45933	Nucleotide sequenc
23	2034.2	18.2	6253	20	AAZ08454	AAV vector sequenc
24	2034.2	18.2	6280	20	AAZ08455	AAV vector sequenc
25	2034.2	18.2	6280	20	AAZ08456	AAV vector sequenc
26	2034.2	18.2	6565	21	AAZ45925	Nucleotide sequenc
27	2034.2	18.2	6565	22	AAF55126	Nucleotide sequenc
28	2034.2	18.2	6708	21	AAC68295	R15/APPA plasmid c
c 29	2034.2	18.2	6714	21	AAZ45930	Nucleotide sequenc
c 30	2034.2	18.2	6898	20	AAV63742	Plasmid UGP232-4 c
c 31	2034.2	18.2	6924	21	AAZ45934	Nucleotide sequenc
c 32	2034.2	18.2	6924	21	AAZ45935	Nucleotide sequenc
33	2034.2	18.2	6971	22	AAF55124	Nucleotide sequenc
34	2034.2	18.2	6981	21	AAZ45931	Nucleotide sequenc
35	2034.2	18.2	7054	21	AAZ45927	Nucleotide sequenc
36	2034.2	18.2	7405	21	AAZ45926	Nucleotide sequenc
37	2034.2	18.2	7492	21	AAZ45929	Nucleotide sequenc
38	2034.2	18.2	7558	22	AAF55125	Nucleotide sequenc
39	2034.2	18.2	7566	14	AAQ42160	Plasmid pPS0212 co
40	2034.2	18.2	7639	14	AAQ42159	Plasmid pJD884 con
41	2034.2	18.2	7914	22	AAF84548	Plasmid DLZ7 encod
42	2034.2	18.2	7944	22	AAF84647	Plasmid DLZ6 encod
43	2034.2	18.2	7969	22	AAF55123	Nucleotide sequenc
c 44	2034.2	18.2	8630	21	AAZ24041	Retroviral M4 mdr-
c 45	2034.2	18.2	8630	21	AAZ24042	Retroviral vector

ALIGNMENTS

RESULT 1  
AAZ47807  
ID AAZ47807 standard; DNA; 11206 BP.  
XX  
AC AAZ47807;  
XX  
DT 10-MAR-2000 (first entry)  
XX  
DE Vector for trapping an unknown gene of Drosophila melanogaster.  
XX  
KW Gene trapping; Drosophila melanogaster; cloning; functional analysis;  
KW artificial consensus splicing acceptor site; reporter gene;  
KW drug resistance gene; detection; splicing donor site; ss.  
XX  
OS Synthetic.  
OS Drosophila melanogaster.  
XX  
PN WO9961604-A2.  
PD  
PD 02-DEC-1999.  
XX  
PF 21-MAY-1999; 99WO-JP02683.  
XX  
PR 22-MAY-1998; 98JP-0141952.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Lukacsovich T, Asztalos Z, Yamamoto D, Awano W;  
XX WPI; 2000-062708/05.  
DR  
XX New gene trapping vector for Drosophila melanogaster genes, used for

PT



PT the cloning and functional analysis of novel genes -  
XX Claim 4; Page 15-21; 35pp; English.

CC The present sequence represents the nucleotide sequence of a specifically  
CC claimed vector for trapping an unknown gene of Drosophila melanogaster  
CC (DM), where the vector is a recombinant plasmid comprising the following  
CC nucleotide sequences in order: (1) an artificial consensus splicing  
CC acceptor site; (2) a synthetic stop/start sequence; (3) a reporter gene;  
CC (4) a drug resistance gene; (5) a gene responsible for a detectable  
CC phenotype of the DM; and (6) a synthetic splicing donor site. The vector  
CC can be used for the cloning and functional analysis of new genes of DM.

XX Sequence 11206 BP; 2998 A; 2648 C; 2564 G; 2996 T; 0 other;

Query Match 100.0%; Score 11206; DB 21; Length 11206;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 11206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgatgaaataacataaggtggtcccgctcggaagagacatccacttaacgtatgcttg 60  
DB 1 catgatgaaataacataaggtggtcccgctcggaagagacatccacttaacgtatgcttg 60

QY 61 caataagtcgcagtgaaaggaatagattctgagtgctcgtattgagtcctgagtcgagacag 120  
DB 61 caataagtcgcagtgaaaggaatagattctgagtgctcgtattgagtcctgagtcgagacag 120

QY 121 cgatatgattgttgattaacccttagatgtccgtggaaggaatggaattaaactcataatt 180  
DB 121 cgatatgattgttgattaacccttagatgtccgtggaaggaatggaattaaactcataatt 180

QY 181 aattagacgaaattattttaaaagttttatttttaataaatttgcgagtcacgaaagctct 240  
DB 181 aattagacgaaattattttaaaagttttatttttaataaatttgcgagtcacgaaagctct 240

QY 241 ttctcttacaggtcgaattgatgtgatggatcccaatgaagctactgtctcttatcgaaaca 300  
DB 241 ttctcttacaggtcgaattgatgtgatggatcccaatgaagctactgtctcttatcgaaaca 300

QY 301 agcatgcgatattttgcgcgacttaaaaagctcaagtgctccaaaagaaaaacggaagtgcg 360  
DB 301 agcatgcgatattttgcgcgacttaaaaagctcaagtgctccaaaagaaaaacggaagtgcg 360

QY 361 caagtgtctgaagaacaactgggagtgctgctactctccaaaacccaaaagggtctccgct 420  
DB 361 caagtgtctgaagaacaactgggagtgctgctactctccaaaacccaaaagggtctccgct 420

QY 421 gactagggcacatctgacagaagtgggaatcaaggctagaagaactggaacagctatttct 480  
DB 421 gactagggcacatctgacagaagtgggaatcaaggctagaagaactggaacagctatttct 480

QY 481 actgatttttcctcgagaagacccttgacatgattttgaaaaatggattctttacaggatat 540  
DB 481 actgatttttcctcgagaagacccttgacatgattttgaaaaatggattctttacaggatat 540

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DB 541 aaaagcattgttaacaggattattttgtacaagataatgtgaataaagatgccgtcacaga 600

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DB 601 tagattggcttcagtgagactgatcgctctaacattgagacagcatagaataagtgc 660

QY 661 gacatcatcatcggagagagtagtaacaaaggtcacaagcagttgactgtatcgattga 720  
DB 661 gacatcatcatcggagagagtagtaacaaaggtcacaagcagttgactgtatcgattga 720

QY 721 ctgcgcagctcatcatgataactccacaattccgctggatttttatgcccagggtgctct 780  
DB 721 ctgcgcagctcatcatgataactccacaattccgctggatttttatgcccagggtgctct 780

QY 781 tcatggatttgattggtctggaaggatgacatgctcggtggtgcttgccttctctgaaaaac 840

DB 781 tcatggatttgattggtctggaaggatgacatgctcggtgcttgccttctctgaaaaac 840

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DB 841 ggaccccaacaataatgggttcttttggcagcggttctctcttatgtattcttgcgactctat 900

QY 901 tggctttaaacccggaataattacacgaactctaacgttaacaggctcccgcacattgattac 960  
DB 901 tggctttaaacccggaataattacacgaactctaacgttaacaggctcccgcacattgattac 960

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DB 961 ggatagatacacogttggcttctagatccacaacatcccgttttacttcaaaagttaattctcaa 1020

QY 1021 taattttcacccctactgcccctatctgctgcaactcaccgacgctaataatgatgttgtataataa 1080  
DB 1021 taattttcacccctactgcccctatctgctgcaactcaccgacgctaataatgatgttgtataataa 1080

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QY 1141 tggagcctgggtgtatagagggggaatctactgatataagatgttttttactatacaaaatgc 1200  
DB 1141 tggagcctgggtgtatagagggggaatctactgatataagatgttttttactatacaaaatgc 1200

QY 1201 taaatctcatgtgacgagcaaggtctcttcgagtcagggttccataaattttggtgacagccct 1260  
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QY 1261 acatctctctgctgcgatacacacagtgggagcagaaaaaataactagctataattttca 1320  
DB 1261 acatctctctgctgcgatacacacagtgggagcagaaaaaataactagctataattttca 1320

QY 1321 cagcttttccataaagaatggccatatcatctgggcttgaaatagggaacctcccctcgctcctt 1380  
DB 1321 cagcttttccataaagaatggccatatcatctgggcttgaaatagggaacctcccctcgctcctt 1380

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QY 1441 gatccaatgtccctgcttattatggtcgatccatccagcttttccagaatacataatctcctt 1500  
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QY 1741 caatttgttgaaggaaacacccttggctatccctttacaagaattgcgaactgaagtggaaaca 1800  
DB 1741 caatttgttgaaggaaacacccttggctatccctttacaagaattgcgaactgaagtggaaaca 1800

QY 1801 gttgtctcttatcatttatgtattaaagagattttttcactaatttttaccagaaaaagtc 1860  
DB 1801 gttgtctcttatcatttatgtattaaagagattttttcactaatttttaccagaaaaagtc 1860

QY 1861 acaactagaacaggatcaaaaatgatcatcaaaagttaagaagttaaacgatgctccatcat 1920

Db 1861 acaactagaacaggatcaaaaatgatcatcaaaagtatatgaagttaaaacgagtctccatcat 1920

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Db 4021 aatggcgaggtagccggatcaagcgtatgcgcgcgcgcgcatttcgcttggtggtcg 4080





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QY 6541 tccgtcagcaaatgtcagcacacgatcatcgggtgcgccggcaggggtgaaaaggctctgtcc 6600

Db 6541 tccgtcagcaaatgtcagcacacgatcatcgggtgcgccggcaggggtgaaaaggctctgtcc 6600

QY 6601 ggcgagaaaaggagcgtctggcattcgccctccgagggcaactaaaccgatccgcgcttctg 6660

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QY 6661 atctcgatgagcccacctccgactggactcatttacgccccacagcgtcgtccagggtg 6720

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QY 11161 gccagatgcgagcaccccggaagctcacgatgagaatggccagac 11206  
Db 11161 gccagatgcgagcaccccggaagctcacgatgagaatggccagac 11206

RESULT 2  
AAQ61607

ID AAQ61607 standard; DNA; 2646 BP.  
XX  
AC AAQ61607;  
XX  
DT 24-NOV-1994 (first entry)  
XX  
DE Mutated GAL4 gene coding for Asp insertion between Asp863 and Val864.  
XX  
KW Mutated GAL4; heterologous gene expression; enhanced; increased;  
KW protein production; positive regulator; transcription activator;  
KW galactose metabolism; ss.  
XX  
OS Eukaryota.  
XX  
FH  
FT mat\_peptide 1..2646  
FT /\*tag= a  
FT /product= mutated\_GAL4  
FT /transl\_except= (pos:190..192, aa:Lys)  
FT /transl\_except= (pos:757..759, aa:Ser)  
FT /transl\_except= (pos:1375..1377, aa:Glu)  
FT /transl\_except= (pos:1990..1992, aa:Cys)  
XX  
PN JP06078767-A.  
XX  
PD 22-MAR-1994.  
XX  
PF 07-SEP-1992; 92JP-0262723.  
XX  
PR 07-SEP-1992; 92JP-0262723.  
XX  
PA (GREC ) GREEN CROSS CORP.

XX WPI; 1994-131274/16.  
DR P-PSDB; AAR51930.  
XX  
PT Mutated GAL4 and a method for the expression of foreign protein -  
PT useful for enhancing expression of protein  
XX Claim 2; Page 13-14; 20pp; Japanese.  
XX  
CC This DNA sequence codes for GAL4 in which an Asp residue is inserted  
CC between wild-type Asp863 and Val864. The mutated GAL4 can be used  
CC for increasing the expression of foreign genes under the control of  
CC the GAL1, GAL7 or GAL10 promoters.  
XX  
SQ Sequence 2646 BP; 825 A; 583 C; 498 G; 740 T; 0 other;  
  
Query Match 23.5%; Score 2628.4; DB 15; Length 2646;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2642; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
  
QY 275 atgaagctactgtcttctatcgaacaagcatcgcatatttgcgacttaaaaagctcaag 334  
Db 1 atgaagctactgtcttctatcgaacaagcatcgcatatttgcgacttaaaaagctcaag 60  
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Db 241 ttgaaaatggattcttttacaggatataaaaagcattgttaacaggattatttgtacaagat 300  
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QY 1055 ccgacgcgctaagtgttggtataataaacacagattgaaatcgcgtcgaaggatcaatggcaa 1114  
Db 781 ccgacgcgctaagtgttggtataataaacacagattgaaatcgcgtcgaaggatcaatggcaa 840  
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RESULT 3  
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ID ABL05134 standard; cDNA; 7869 BP.  
XX  
AC ABL05134;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9884.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX



QY 7357 ttttcaatgagatgtatatagtttatagtttttcagaaaaataaaattttcaatttaactcg 7416  
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|||||  
Db 1403 CCAGTATACCTCAAATGGTTGTGCTACCTCTCATGGTTCGGTTACGCCAACGAGGGTCTG 1344  
QY 8077 ctgattaaacaaatggcggacgtggagccggcgaaatttagctgcacatcgtcgaacacc 8136  
|||||  
Db 1343 CTGATTAAACCAATGGCGGACGTGGAGCCGGCGGAAATTAGCTGCACATCGTCGAACACC 1284  
QY 8137 acgtgccccagttcgggcaagggtcatccttgagacgcttaacttctccgcgcgcgatctg 8196  
|||||  
Db 1283 ACGTGCCCCAGTTTCGGGCAAGGTCAATCTCTGGAGACGCTTAACTTCTCCGCCGCCGATCTG 1224  
QY 8197 ccgctggactacgtgggtcttgccattctcatcgtgagcttccgggtgctcgcatatctg 8256  
|||||  
Db 1223 CCGCTGGACTACGTGGGTCTGGCCATTCTCATCGTGAGCTTCCGGGTGCTCGCATATCTG 1164  
QY 8257 gctctaagacttcggggcccgacgcaagaggtagaaggttagcggccgcacgtaaggg 8316  
|||||  
Db 1163 GCTTAAGACTTCGGGCCCGACGCAAGGAGTAGCCGACATATATCCGAAATAACTGCTGTTG 1104  
QY 8317 ttaatgttttca 8328  
|||  
Db 1103 TTTTTTTITTTTA 1092

RESULT 4  
AAX57224  
ID AAX57224 standard; DNA; 7286 BP.

XX AAX57224;  
AC  
XX  
DT 26-JUL-1999 (first entry)  
XX  
DE WO 9923223 Seq ID 2.  
XX  
KW Inducible promoter; invertase; catabolite inhibition; vector;  
extracellular expression; foreign gene; regulation expression; ss.  
XX Schizosaccharomyces pombe.  
OS  
XX WO9923223-A1.  
XX  
PD 14-MAY-1999.  
XX  
PF 30-OCT-1998; 98WO-JP04929.  
XX  
PR 31-OCT-1997; 97JP-0314608.  
XX  
PA (ASAG ) ASAHI GLASS CO LTD.  
XX  
PI Hama Y, Kumagai H, Tohda H;  
XX  
DR WPI; 1999-313344/26.  
XX  
PT Promoter and secretory signal sequences from invertase gene of  
Schizosaccharomyces pombe  
XX  
PS Disclosure; Page 52-57; 67pp; Japanese.  
XX  
CC This invention describes a novel promoter region of the moiety relating  
to catabolite inhibition of the invertase gene of Schizosaccharomyces  
pombe. The products of the invention can be used in the construction of  
a vector which allows extracellular expression of a foreign gene,  
regulated by the presence or absence of a specific nutrient such as  
glucose and results in the easy regulated expression of foreign genes  
in a yeast system.  
XX  
SQ Sequence 7286 BP; 2181 A; 1557 C; 1544 G; 2004 T; 0 other;

Query Match 18.8%; Score 2102.8; DB 20; Length 7286;  
Best Local Similarity 59.1%; Pred. No. 0;  
Matches 4167; Conservative 0; Mismatches 2732; Indels 155; Gaps 27;  
QY 3575 ggcaggttggcgtcgcttggctgcgtcatttcgaacccacagagtcgccgcagaagaact 3634  
|||||  
Db 209 ggcaggttggcgtcgcttggctgcgtcatttcgaacccacagagtcgccgcagaagaact 268  
QY 3635 cgtcaagaagcgcatagaagcgcatgcgtcgcgaatcgggagcgcgataccgtaaaagca 3694  
|||||  
Db 269 cgtcaagaagcgcatagaagcgcatgcgtcgcgaatcgggagcgcgataccgtaaaagca 328  
QY 3695 cgaggagcggtcagcccatcgcgcgccaaagctcttcagcaatatcacgggtagccaacg 3754  
|||||  
Db 329 cgaggagcggtcagcccatcgcgcgccaaagctcttcagcaatatcacgggtagccaacg 388  
QY 3755 ctatgtcctgatagcggttcgcgcacacaccccgccacagtcgatgaatccagaaaaagc 3814  
|||||  
Db 389 ctatgtcctgatagcggttcgcgcacacaccccgccacagtcgatgaatccagaaaaagc 448  
QY 3815 ggccattttccaccatgatatttcggcaagcagggcatcgccatgggtcacgacgagatcct 3874  
|||||  
Db 449 ggccattttccaccatgatatttcggcaagcagggcatcgccatgggtcacgacgagatcct 508  
QY 3875 cgccgtcgggcacgtcgcccttgagcctggcaaacagttcggctggcgagccccctgat 3934  
|||||  
Db 509 cgccgtcgggcacgtcgcccttgagcctggcaaacagttcggctggcgagccccctgat 568  
QY 3935 gctcttcgtccagatcctcctgatcgcacaagaccggcttccatccgagtagtctcgct 3994  
|||||  
Db 569 gctcttcgtccagatcctcctgatcgcacaagaccggcttccatccgagtagtctcgct 628











Db 7141 catttccccgaaaagtccacctgacgtctctaagaaccattattatcatgacattaacct 7200

QY 10468 ataaaaatagcggtatcacgagggcccttctgtct 10501

Db 7201 ataaaaatagcggtatcacgagggcccttctgtct 7234

RESULT 5

ABA04129/c

ID ABA04129 standard; DNA; 3753 BP.

XX ABA04129;

AC ABA04129;

XX 28-FEB-2002 (first entry)

XX Plasmid pHCE19T(II) polynucleotide sequence SEQ ID NO:3.

DE

XX Promoter; gene expression; fermentation; D-AAT; Bacillus SK-1;

KW D-amino acid aminotransferase; economic; large-scale protein production;

KW circular; ds.

XX Bacillus sp. SK-1.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT promoter 1..223

FT /\*tag= a

FT /note= "specifically claimed promoter region in

FT Claim 1 (see ABA04127)"

XX

PN WO200183787-A1.

XX

XX 08-NOV-2001.

XX

PE 26-APR-2001; 2001WO-JP03607.

XX

XX

PR 27-APR-2000; 2000JP-0128528.

XX

XX (BIOL-) BIOLEADERS CORP.

PA (TAKI ) TAKARA SHUZO CO LTD.

XX

PI Sung M, Lee S, Hong S, Seo H;

XX

DR WPI; 2002-065535/09.

XX

PT Promoter sequence effective in Escherichia coli and Bacillus for

PT economic large-scale fermentative production of proteins -

XX

PS Claim 7; Page 55-57; 65pp; Japanese.

XX

CC The present invention describes a DNA sequence (I) comprising promoter

CC activity in Escherichia coli or Bacillus cells, where the promoter is

CC derived from the D-AAT (D-amino acid aminotransferase) gene of

CC Bacillus SK-1. (I) can be used for the high level expression of a

CC foreign gene in a bacterial host for economic and efficient large-scale

CC production of proteins such as enzymes, cytokines and antibodies. The

CC present sequence represents the plasmid pHCE19T(II) polynucleotide

CC sequence comprising a specifically claimed promoter region from the

CC present invention.

XX

SQ Sequence 3753 BP; 953 A; 912 C; 929 G; 959 T; 0 other;

Query Match 18.2%; Score 2034.2; DB 24; Length 3753;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 8662 agttcaagaagaaggcgtttttcccataggtccgccccctgacgagcatcacaaaaatc 8721

Db 3348 AGGCCGCGTGTGCTGGCGGTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATC 3289

QY 8722 gacgctcaagtcagaggtggtgcgaaacccgacaggaactataaagataccaggcgctttcccc 8781

Db 3288 GACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATACCCAGCGTTTCCCC 3229

QY 8782 ctggaagctccctcgctgcgtctctcctgttccgacccctgcgcttaccggatacctgtccg 8841

Db 3228 CTGGAAGCTCCCTCGTGCCTCTCCTCTGTCGACCCCTGCCGCTTACCGGATACCTGTCCG 3169

QY 8842 cctttctcccttcgggaagcgtggcgctttctcaatgctcacgctgtaggtatctcagtt 8901

Db 3168 CCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACGCTGTAGGTATCTCAGTT 3109

QY 8902 cgggtgtaggtcgttcgctccaagcgtggcgtgtgtgcacgaaccccccgcttcagcccgacc 8961

Db 3108 CGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACC 3049

QY 8962 gctgcgccttataccggtaactatcgcttgagtcaccaacccggtaagacacgacttatcgc 9021

Db 3048 GCTGCGCCTTATCCGTAACATATCGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGC 2989

QY 9022 cactggcagcagccactggtaacaggattagcagagcgaggtatgtaggcggtgctacag 9081

Db 2988 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTACAG 2929

QY 9082 agttcttgaagtgtggcctaactacgctacactagaaagacagtatttgggtatctgcg 9141

Db 2928 AGTTCTTTGAAGTGTGGCCTAACTACGCTACACTAGAAGGACAGTATTTGSTATCTGCG 2869

QY 9142 ctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccggcaaaaaaa 9201

Db 2868 CTCTGCTGAAGCCAGTTACCTTCGGAAGGAGTTGGTAGCTCTTGATCCGGCAAAACAAA 2809

QY 9202 ccaccgctggtagcgggtggtttttttgtttgcaagcagcagattacgcgcagaaaaaaag 9261

Db 2808 CCACCGCTGGTAGCGGTGGTTTTTTGTGTGCAAGCAGCAGATTACGCGCAGAAAAAAG 2749

QY 9262 gatctcaagaagatcccttggatctttctacggggtctgacgctcagtggaacgaaaaact 9321

Db 2748 GATCTCAAGAAGATCCTTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACT 2689

QY 9322 cacgttaagggtatttgggtcatgagattatcaaaaaaggatcttcacctagatccttttaa 9381

Db 2688 CACGTTAAGGGATTGTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAA 2629

QY 9382 attaaaaatgaagttttaaatcaactaaagtatatatagtaaaacttggctgacagtt 9441

Db 2628 ATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTT 2569

QY 9442 accaatgcttaatcagtgaggcacctatctcagcgatctgtctatttcttcattccatag 9501

Db 2568 ACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTCTCTATTTCGTTTCATCCATAG 2509

QY 9502 ttgcctgactccccgctggtagataactacgatacgggagggcttaccatctggcccca 9561

Db 2508 TTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGSGAGGGCTTACCATCTGGCCCCA 2449

QY 9562 gtgctgcaatgataccgcgagacccacgctcacccggtccagatttatcagcaataaaacc 9621

Db 2448 GTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAAC 2389

QY 9622 agccagccgggaaggccgagcgcagaagtggtcctgcgaactttatccgcctccatccagt 9681

Db 2388 AGCCAGCCGGAAGGCCCGAGCGCAGAAAGTGGTCTCTGCAACTTTATCCGCCCTCCATCCAGT 2329

QY 9682 ctatttaattgttgcgggaagctagagtaagttagttcgcaggttaaatagtttgcgcaacg 9741

Db 2328 CTATTAAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCGCAACG 2269

QY 9742 ttgttgccattgctacaggcatcgtggtgtcacgctcgtcgttgggtatggcttcattca 9801

Db 2268 TTGTTGCCATTGCTACAGGCATCGTGGTGTTCACGCTCGTCGTTGGTATGGCTTCATTCA 2209

QY 9802 gctccgggttcccaacgatcaaggcaggttacatgatcccccatgttgtgcaaaaaagcgg 9861

Db 2208 GCTCCGGTTCCCAACGATCAAGCGGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGG 2149

Qy 9862 ttagtcccttcggtcccgatcgttgcagaagtaagtggccgcagtggttatcaactca 9921  
|||||

Db 2148 TTAGCTCCTTCGGTCCTCCGATCGTTGTGAGAAAGTAAGTTGGCCGCAGTGTATCACTCA 2089

Qy 9922 tggttatggcagcactgcataaattctcttactgtcatgccatccgtaagatctttctg 9981  
|||||

Db 2088 TGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCTG 2029

Qy 9982 tgactgggtgagtactcaaccaaagtcatcttgagaatagtgtatcgcgcgacgagttgct 10041  
|||||

Db 2028 TGACTGGTGAGTACTCAACCAAGTCAATTCTGTGAGAAATAGTGTATGCGCGCAGCGAGTTGCT 1969

Qy 10042 cttgcocggcgtcaacacgpggataataaccgcgcacatagcagaactttaaagtgctca 10101  
|||||

Db 1968 CTTGCCCGCGCTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGTCTCA 1909

Qy 10102 tcatggaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 10161  
|||||

Db 1908 TCATTGGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCCTGTTGAGATCCA 1849

Qy 10162 gttgatgttaaccactcgtgcaccccaactgatcttcagcatcttttacttttcaaccagcg 10221  
|||||

Db 1848 GTTCGATGTAACCCACTCGTGCACCCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCG 1789

Qy 10222 tttctgggtgagcaaaacaggaaggcaaaatgccgcaaaagggaataaaggcgacac 10281  
|||||

Db 1788 TTTCTGGGTGAGCAAAAACAGGAAGGCAAAAATGCCGCAAAAAGGGAATAAGGGCGACAC 1729

Qy 10282 ggaatgttgaatactcatactctctcccttttcaatattattgaagcatttatcagggtt 10341  
|||||

Db 1728 GGAATGTGTAATACTACTACTCTTCCTTTTCAATATTATTGAAGCATTTATCAGGGTT 1669

Qy 10342 attgtctcatgagcggatcacatatatttgaatgtatttagaaaaataaacaataagggttc 10401  
|||||

Db 1668 ATTGCTCATGAGCGGATACATATTTGAAATGTATTTAGAAAAATAAACAAATAGGGGTT 1609

Qy 10402 cgcgcacatttccccgaaaagtgccacctgacgtctaagaaacattattatcatgacat 10461  
|||||

Db 1608 CGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATATTATTATCATGACAT 1549

Qy 10462 taacctataaaaaataggcgtatcacgagggcccttctcgtcgcgcgttctcgtgatgacg 10521  
|||||

Db 1548 TAACTATAAAAAATAGCGGTATCACGAGGCGCTTTCGTCTCGCGCTTTCGGTGATGACG 1489

Qy 10522 gtgaaaacctctgacacatgcagctcccgagacgggtcacagcttctgttaagcggatg 10581  
|||||

Db 1488 GTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCAACAGCTTGCTGTGAAGCGGATG 1429

Qy 10582 ccgggagcagacaagcccgtcagggcgcgtcagcgggtgttgcggggtgcgggctggc 10641  
|||||

Db 1428 CCGGGAGCAGACAAAGCCCGTCAGGGCGCGTcAGCGGGTGTGGCGGGTGTTCGGGGCTGGC 1369

Qy 10642 ttaactatgcggcatcagagcagattgtactgagagtgcaccatatgcgggtgtgaaatac 10701  
|||||

Db 1368 TTAACCTATCGGGCATCAGAGCAGATTGTACTGTAGAGTGCACCATATGCGGTGTGAAATAC 1309

Qy 10702 cgcaccgaatcgcgcgggaactaa 10724  
|||||

Db 1308 CGCACAGATGCGTAAGGAGAAAA 1286

RESULT 6

ABA04130/c

ID ABA04130 standard; DNA; 3755 BP.

XX

AC ABA04130;

XX

DT 28-FEB-2002 (first entry)

XX

DE Plasmid pHCE19(II) polynucleotide sequence SEQ ID NO:4.

XX

KW Promoter; gene expression; fermentation; D-AAT; Bacillus SK-1;  
KW D-amino acid aminotransferase; economic; large-scale protein production;  
KW circular; ds.

XX

OS Bacillus sp. SK-1.  
OS Synthetic.

XX

FH Key Location/Qualifiers  
FT promoter 1..225  
FT /\*tag= a  
FT /note= "specifically claimed promoter region in  
FT Claim 1 (see ABA04128)"

XX

PN WO200183787-A1.

XX

PD 08-NOV-2001.

XX

PF 26-APR-2001; 2001WO-JP03607.

XX

PR 27-APR-2000; 2000JP-0128528.

XX

PA (BIOL-) BIOLEADERS CORP.  
PA (TAKI ) TAKARA SHUZO CO LTD.

XX

PI Sung M, Lee S, Hong S, Seo H;

XX

DR WPI; 2002-066535/09.

XX

PT Promoter sequence effective in Escherichia coli and Bacillus for  
PT economic large-scale fermentative production of proteins -

XX

PS Claim 7; Page 58-60; 65pp; Japanese.

XX

CC The present invention describes a DNA sequence (I) comprising promoter  
CC activity in Escherichia coli or Bacillus cells, where the promoter is  
CC derived from the D-AAT (D-amino acid aminotransferase) gene of  
CC Bacillus SK-1. (I) can be used for the high level expression of a  
CC foreign gene in a bacterial host for economic and efficient large-scale  
CC production of proteins such as enzymes, cytokines and antibodies. The  
CC present sequence represents the plasmid pHCE19(II) polynucleotide  
CC sequence comprising a specifically claimed promoter region from the  
CC present invention.

XX

SQ Sequence 3755 BP; 951 A; 914 C; 932 G; 958 T; 0 other;

Query Match 18.2%; Score 2034.2; DB 24; Length 3755;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 8662 agttcaagaagaagcggtttttccataggctccgcccccctgacgagcatcacaaaaatc 8721  
|||

Db 3350 AGGCCGCGTTGCTGCGGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC 3291

Qy 8722 gaogctcaagtcagaggtggcgaaacccgcacaggactataaagataccaggcgtttcccc 8781  
|||||

Db 3290 GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC 3231

Qy 8782 ctggaagctccctcgtgcgtctctcctgttccgacccctgcgcttaccggataacctgtccg 8841  
|||||

Db 3230 CTGGAAGCTCCCTCGTGGCTCTCCCTGTCGACCCCTGCGCTTACCGGATACCTGTCCG 3171

Qy 8842 cctttctcccttcgggaagcgtggcgctttctcattcgaatgctaggtatctcagtt 8901  
|||||

Db 3170 CTTTCTCCCTTCGGGAAGCGGTGGCGCTTCTCTCAATGCTACGCTGTAGGTATCTCAGTT 3111

Qy 8902 cgggtaggtcgttcgctccaagctggcgtgtgtgcacgaaccccccggttcagccgacc 8961  
|||||

Db 3110 CGGTGTAGGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTACGCCCGACC 3051

Qy 8962 gctgcgccttatccggttaactatcgttcttgagtcacacccggtaagacacgacttatcgc 9021  
|||||

Db 3050 GCTGCGCCTTATCCGTTAACTATATCGTCTTGAGTCCAACCCGTTAAGACACGACTTATCGC 2991

QY 9022 cactgagcagccactggttaacaggattagcagagcagaggtatgttagcggtgtctaacg 9081  
Db 2990 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGGAGGTATGTAGGCGGTGCTACAG 2931  
QY 9082 agttcttgaaagtgtggtcctaactacggtctacactagaaaggacagtagtttgggtatctg 9141  
Db 2930 AGTTCCTGAAGTGGTGCCCTAACTACGCTACACTAGAGGACAGTATTGGGTATCTGCG 2871  
QY 9142 ctctgctgaagccaggttaccttcggaataagagttggtagctcttgatccgggcaaaacaa 9201  
Db 2870 CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAA 2811  
QY 9202 ccaccgctggtagcggtggttttttctggtttgcaagcagcagattacgcgcagaaaaaag 9261  
Db 2810 CCACCGCTGGTAGCGGTGGTGTTCCTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAG 2751  
QY 9262 gatctcaagaagatcccttttgatccttttctacggggtctgaagcgtcagtggaacgaaaa 9321  
Db 2750 GATCTCAAGAAGATCCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGGACGAAAACT 2691  
QY 9322 cactgtaagggtatttgggtcatgagattatcaaaaaaggtcttcacctagatcccttttaa 9381  
Db 2690 CACGTTAAGGGATTGTGGTCATGAGATTATCAAAAAAGGATCTTCACCTAGATCCTTTTAA 2631  
QY 9382 attaaaaatgaagttttaaatcaatcaactaaagtatatatagtagtaaaacttggctgacagt 9441  
Db 2630 ATTAAAAATGAAGTTTAAATCAATCTAAAAAGTATATATAGATAAACCTTGGTCTGACAGTT 2571  
QY 9442 accaatgcttaatacagtgagcaccctatctcagcgatctgtctatatttcgttccatccatag 9501  
Db 2570 ACCAATGCTTAATCAGTGAGGCACCCCTATCTCAGCGATCTGTCTATTTCGTTTCATCCATAG 2511  
QY 9502 ttgctgactccccctgctgttagataaactacgatacgggaggggttaccatctggcccca 9561  
Db 2510 TTGCTTGACTCCCCGTCGTGTAGATAAATACTACGATACGGGAGGGCTTACCATCTGGCCCCA 2451  
QY 9562 gtgctgcaatgatataccgcgagaccccgctcaccggtccagatttatcagcaataaacc 9621  
Db 2450 GTGCTGCAATGATACCGCGGAGACCCACGCTCACCGGCTCCAGATTATACAGCAATAAACC 2391  
QY 9622 agccagccggaaggccgagcgcagaagtgctcctgcaactttatccgcctccatccagt 9681  
Db 2390 AGCCAGCCGGAAAGGCCGAGCGCAGAGAGTGGTCTCTGCAACTTTATCCGCCCTCCATCCAGT 2331  
QY 9682 ctattaattgttgcggggaagctagagtaagttagtcgcagtttaatagtttgcgcaacg 9741  
Db 2330 CTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCGCAACG 2271  
QY 9742 ttgttgccattgctacaggcatcgtggtgtcagcgtcgttgggttgggtatggcttcattca 9801  
Db 2270 TTGTTGCCATTGCTACAGGCATCGTGGTGTCAACGCTCGTCTGTTGGTATGGCTTCATTCA 2211  
QY 9802 gctccggttcccaacgatcaaggcgaggttacatgatcccccatgttgtgcaaaaaaagcgg 9861  
Db 2210 GCTCCGGTTCCCAACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAAGCGG 2151  
QY 9862 ttagctccttcggtccctccgatacgttgtcagaagtaagttggcgcagtggttatcactca 9921  
Db 2150 TTAGCTCCTTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGACAGTGTATCACTCA 2091  
QY 9922 tggttatggcagcactgcataaattctcttactgtcatgccatccgtaagatgcttttctg 9981  
Db 2090 TGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATGCCATCCGTAAGATGCTTTTCTG 2031  
QY 9982 tgactggtgagtactcaaccaagtcattcttgagaatagtgtagtcggcgaccgaggttgc 10041  
Db 2030 TGACTGGTGAGTACTCAACCAAGTCATCTTGAGAAATAGTGTATGCGCGCACCAGTTGCT 1971  
QY 10042 ctgcccggcgctcaacacgggataataaccgcgccacatagcagaactttaaaagtgtca 10101  
Db 1970 CTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTTAAAGTGCTCA 1911

QY 10102 tcattgaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 10161  
Db 1910 TCATTGGAANAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCA 1851  
QY 10162 gttecatgtaacccactcgtgcaccccaactgatcttcagcatcttttactcttcaccagcg 10221  
Db 1850 GTTCGATGTAAACCCACTCGTGCACCCCACTGATCTTTCAGCATCTTTTACTTTCAACCAGCG 1791  
QY 10222 tttctgggtgagcaaaaacaggaagggcaaaatgccgcaaaaagggaataaaggcgacac 10281  
Db 1790 TTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGAATAAAGGCGGACAC 1731  
QY 10282 ggaaatgttgaatactcatactcttcccttttcaatatatttgaagcatttatcaggggtt 10341  
Db 1730 GGAAATGTTGAATACTCATACTCTTCCCTTTTCAATATATTGAAGCATTTTATCAGGGTT 1671  
QY 10342 attgtctcatgagcgggatacatatttgaatgtatttagaaaaataaacaataggggttc 10401  
Db 1670 ATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTTC 1611  
QY 10402 cgcgcacatttccccgaaaagtgccacctgacgtctaaagaaccattattatcatgacat 10461  
Db 1610 CGCGCACATTTCGCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTTATTATCATGACAT 1551  
QY 10462 taacctataaaaataggcgtatcacaggagcccttctcgtcgcgcttctcggtgatgacg 10521  
Db 1550 TAACCTATAAAAATAGCGGTATCACGAGGCCCTTTCGTCTCGCGCGTTCGGTGTATGACG 1491  
QY 10522 gtgaaaaacctctgacacatgcagctccccggagacgggtcacagcttctgttaagcggtatg 10581  
Db 1490 GTGAAAACTCTTGACACATGCAGCTCCCCGGAGACGGTCAACAGCTTGTCTGTAAAGCGGATG 1431  
QY 10582 ccgggagcagacaaagcccgctcagggcgcgctcagcggtgttggcggtgtcggtggctggc 10641  
Db 1430 CCGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTCTCGGGCTGGC 1371  
QY 10642 ttaactatgcggcatcagagcagattgtactgagagtgccaccatatgcggtgtgaaatac 10701  
Db 1370 TTAACATATCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATAC 1311  
QY 10702 cgcaccgaatcgcgcggaactaa 10724  
Db 1310 CGCACAGATCGGTAAGGAGAAAA 1288  
RESULT 7  
AAV12067/c  
ID AAV12067 standard; cDNA; 4713 BP.  
XX  
AC AAV12067;  
XX  
DT 08-JUN-1998 (first entry)  
XX  
DE Murine IAD alpha chain cDNA.  
XX  
KW Major histocompatibility class II antigen; MHC class II; T cell;  
KW T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell;  
KW APC; autoimmune disease; diabetes; multiple sclerosis;  
KW autoimmune thyroiditis; systemic lupus erythromatosus;  
KW myasthenia gravis; Crohn's disease; inflammatory bowel disease;  
KW allergy; asthma; contact sensitivity; immunotherapy; therapy;  
KW IAD alpha chain; mouse; ds; circular; cyclic.  
XX  
OS Mus musculus.  
XX  
PN WO9746256-A1.  
XX  
PD 11-DEC-1997.  
XX  
PF 22-MAY-1997; 97WO-US08697.  
XX  
PR 23-MAY-1996; 96US-0018175.  
XX





Db 2760 TTTCTGGGTGAGCAAAACAGGAAGGCANAATGCCGCAAAAAGGAATAAGGGCGACAC 2701  
QY 10282 ggaatgttgaaatactactctctctcttttcaatattattgaagcatttatcagggtt 10341  
Db 2700 GGAATGTTGAATACTCATACTCTTCTCTTTTCAATATTATTGAAGCATTTATCAGGGTT 2641  
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QY 10462 taactataaaaatagcggtatcacgagggcccttctcgtcgcggttccggtgatgacg 10521  
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QY 10522 gtgaaaacctctgacacatgcagctcccgagagacgggtcacagcttctgttaagcggatg 10581  
Db 2460 GTGAAAACCTCTGACACATGCAGTCTCCCGAGACGGTTCACAGCTTGCTGTGAAGCGGATG 2401  
QY 10582 ccggagagcagacaagccgctcagggcgcggtcagcgggtgttgcggggtgcgggctggc 10641  
Db 2400 CCGGAGCAGACAAGCCCGTCAAGGCGCGTCAGCGGGGTGTTCGGGGCTGGC 2341  
QY 10642 ttaactatcgggcatcagagcagattgtactgagagtgcacatatgcggtgtgaaatac 10701  
Db 2340 TTAAGTATCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATAC 2281  
QY 10702 cgcaccgaatcgcgcggaactaa 10724  
Db 2280 CGCACAGATGCGTAAGGAGAAAA 2258

RESULT 8  
AAV12068/c  
ID AAV12068 standard; cDNA; 4724 BP.  
XX  
AC AAV12068;  
XX  
DT 08-JUN-1998 (first entry)  
XX  
DE Murine IAD beta chain cDNA.  
XX  
KW Major histocompatibility class II antigen; MHC class II; T cell;  
KW T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell;  
KW APC; autoimmune disease; diabetes; diabetes; multiple sclerosis;  
KW autoimmune thyroiditis; systemic lupus erythromatosus;  
KW myasthenia gravis; Crohn's disease; inflammatory bowel disease;  
KW allergy; asthma; contact sensitivity; immunotherapy; therapy;  
KW IAD beta chain; mouse; ds; circular; cyclic.  
XX  
OS Mus musculus.  
XX  
PN WO9746256-A1.  
XX  
PD 11-DEC-1997.  
XX  
PF 22-MAY-1997; 97WO-US08697.  
XX  
PR 23-MAY-1996; 96US-0018175.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Jackson MR, Karlsson L, Peterson PA, Webb SR, Winqvist O;  
XX  
DR WPI; 1998-041895/04.  
XX  
PT Synthetic antigen presenting cell for activating CD4+ T cells -  
PT useful to treat autoimmune disease, e.g. diabetes, multiple  
PT sclerosis, Crohn's disease and inflammatory bowel disease, or

PT allergy, e.g. asthma and contact sensitivity  
XX  
PS Example 2; Page 94-96; 14lpp; English.  
XX  
CC This nucleotide sequence comprises a PCR product obtained by  
CC amplification of mouse splenocyte cDNA using primers (see AAV12065  
CC and AAV12066) designed for the amplification of IAD beta chain  
CC full-length cDNA. IAD alpha chain cDNA (see AAV12067) has been  
CC similarly obtained. The IAD sequences were cloned into  
CC metallothionein promoter (see AAV12062)-driven vector prnHa-3  
CC prior to sequencing. Major histocompatibility complex (MHC) class  
CC II IAD heterodimers were expressed at the cell surface of  
CC transfected Drosophila Schneider 2 (ATCC CRL 10974) cells. The  
CC invention relates to the preparation and use of synthetic antigen  
CC presenting matrices, in particular antigen presenting cells such as  
CC insect cells that have been transfected to produce MHC antigen  
CC presenting molecules with one or more accessory molecules. The  
CC matrices are used to activate naive CD4+ T cells and to shift the  
CC ongoing activation state into a preferred differentiated population  
CC of Th1 or Th2 cells. Applications include the treatment of  
CC autoimmune disease, e.g. diabetes, multiple sclerosis, autoimmune  
CC thyroiditis, systemic lupus erythematosis, myasthenia gravis,  
CC Crohn's disease and inflammatory bowel disease, or an allergy, e.g.  
CC asthma and contact sensitivity.  
XX  
SQ Sequence 4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 other;

Query Match 18.2%; Score 2034.2; DB 19; Length 4724;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 8662 agttcaagaagaagcggtttttccataggtctcgcccccttgacgagcatcaaaaaatc 8721  
Db 4331 AGGCCGCGTTGCTGGCGTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATC 4272  
QY 8722 gacgctcaagtcagaggtggcgaaacccgacaggaactataaagataccaggcggtttccc 8781  
Db 4271 GACGCTCAAGTCAGAGGTGGCGAACCACGACAGGACTATAAAGATACCAGCGGTTCCCC 4212  
QY 8782 ctggaagctccctcgtgcgtctcctgttccgacctgcgcgttaccggataacctgtccg 8841  
Db 4211 CTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCCCTGCCGTTACCGGATACCTGTCCG 4152  
QY 8842 cctttctcccttcgggaagcggtggcgcttttctcaatgctcacgctgtaggtatctcagtt 8901  
Db 4151 CCTTCTCCCTTCGGGAAGCGGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTT 4092  
QY 8902 cgggtgtagtgcgtcgtccaaagctgggctgtgtgcacgaaccccccttcagcccgacc 8961  
Db 4091 CGGTGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCGACC 4032  
QY 8962 gctgcgccttaccggtaactatcgttcttgagtcacacccggtaagacacgacttatcgc 9021  
Db 4031 GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC 3972  
QY 9022 cactggcagcagccactggtaacaggattagcagagagggtatgtaggcggtgctacag 9081  
Db 3971 CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAG 3912  
QY 9082 agttcttgaagtgtggcctaactacggtctacactagaaggacagtagtatttggtatctgcg 9141  
Db 3911 AGTTCTTGAAGTGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTCGG 3852  
QY 9142 ctctgctgaagccaggttaccttcggaaaaaagagttgtagctcttgatcccgcaaaaaa 9201  
Db 3851 CTCTGCTGAAGCCAGTTACCTTCGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAA 3792  
QY 9202 ccaccgctgtagcggtgtgtttttttgttgcagaagcagagattacgcgcagaaaaaag 9261  
Db 3791 CCACCGCTGTTAGCGGTGGTGTGTGTTCGAAGCAGCAGATTACGCGCAGAAAAAAG 3732  
QY 9262 gatctcaagaagatccctttgatcttttctacgggggtctgacgctcagtggaacgaaaaact 9321









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FT /note= "CDS 8"  
FT 1759..1803  
FT / \*tag= i  
FT /note= "CDS 9"  
FT 1840..1887  
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FT 1911..1961  
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FT 1967..1981  
FT / \*tag= l  
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FT 1990..2010  
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FT /note= "CDS 13"  
FT 2061..2099  
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FT /note= "CDS 14"  
FT 2157..2237  
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FT 4167..4250  
FT / \*tag= x  
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FT /note= "CDS 27"  
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FT / \*tag= ab  
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FT 4567..4776  
FT / \*tag= ac  
FT /note= "cds 29"

WO9928489-A2.

10-JUN-1999.

XX

PF 27-NOV-1998; 98WO-DE03543.  
XX  
PR 28-NOV-1997; 97DE-1052854.  
XX  
PA (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.  
XX  
PI Cichutek K, Engelstaedter M;  
XX WPI; 1999-371131/31.  
DR  
XX  
PT Cell-specific retroviral vectors with antibody domains suitable for  
PT cell-specific transduction of selected mammal cell types - useful  
PT for vaccination and gene therapy for treatment of, e.g. cystic  
PT fibrosis  
XX  
PS Disclosure; Fig 4A-B; 38pp; German.  
XX  
CC This invention describes the construction of novel cell-specific  
CC retroviral vectors with antibody domains suitable for cell-specific  
CC transduction of selected mammal cell types. The invention describes a  
CC method to produce cell-specific retroviral vectors which consists  
CC essentially of the following steps: (a) immunization of a mammal with  
CC one or more cell populations (b) isolation of RNA from the immunized  
CC mammal, especially the B cell RNA (c) production of a cDNA strand of  
CC the variable region of the heavy and light chains of the immunoglobulins  
CC isolated from the RNA by RT-PCR with primers for the respective  
CC immunoglobulin chains, where the primer nucleic acid sequences are for  
CC an oligopeptide linker (d) ligation of the cDNA strain to scFv-cDNA (e)  
CC ligation of the scFv cDNA in a phagemid vector and transformation of a  
CC host bacterium with the vector (f) isolation of phage, by selection of  
CC phage that bind to the cell population used in step (a) (g) cleavage of  
CC the scFv coding DNA fragments from the cell-specific phage and ligation  
CC into a psi-negative retroviral Env-expression vector (h) transformation  
CC of a Env-ScFv expression vector to be maintained in a packaging cell and  
CC (i) isolation of a packaging cell with the retroviral vectors. The  
CC pseudo-type retroviral vectors with modified surface capsid proteins are  
CC suitable for cell-specific transduction of a selected mammal cell type  
CC (cell targeting). The methods are useful for the production of the  
CC pseudo-type retroviral vectors and for gene transfer in selected cell  
CC types. The vectors can be used in medicaments for gene therapy,  
CC vaccination or diagnosis. They are particularly useful for therapy of  
CC cystic fibrosis, ADA-deficiency, chronic granulomatosis or HIV-1  
CC infection. This sequence represents the expression construct pTC53  
CC which is composed from the SNV ENV protein and a murine derived scFv  
CC fragment. This sequence encodes the protein fragments represented in  
CC AAY08761-Y08790.  
XX  
SQ Sequence 4776 BP; 1199 A; 1178 C; 1245 G; 1154 T; 0 other;

Query Match 18.2%; Score 2034.2; DB 20; Length 4776;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 8722 gacgctcaagtcagagggtggcgaaaccccgacaggactataaagataccaggcgtttcccc 8781  
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QY 8782 ctggaagctccctcgtgcgctctcctgttccgaccctgcgcgttacccgataccctgcg 8841  
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||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 2723 cctttctcccttcgggaagcgtggcgcttttctcaatgctcacgctgtaggtatctcagtt 2782  
QY 8902 cgggtaggtcgttcgtcccaagctgggctgtgtgtgcaagaaccccccttcagccgacc 8961  
||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 2783 cgggtaggtcgttcgtcccaagctgggctgtgtgtgcaagaaccccccttcagccgacc 2842



QY 8962 gctgcgcccttatccggttaactatcgtctcttgagtcacaaccccggttaagcacacgacttatcgc 9021  
Dbb 2843 gctgcgcccttatccggttaactatcgtctcttgagtcacaaccccggttaagcacacgacttatcgc 2902  
QY 9022 cactggcagcagccactcgttaacaggattagcagagcgaggtatgttagcggtgtctacag 9081  
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Dbb 3203 cactgtaagggattttggtcatgagattatcaaaaaaggatcttcaacctagatcccttttaa 3262  
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Dbb 3383 ttgcctgactccccgctcgtgtagataaactacgatacgggaggggttaccatctggcccca 3442  
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Dbb 3443 gtgctgcaatgataccgcgagacccacgctcaccggctccagatttatcagcaataaaacc 3502  
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QY 9682 ctattaatgttgcgggaaagctagagtaagttagttcgcagtttaagtttgcgcaacg 9741  
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QY 10702 cgcaccggaatcgcgcgggaactaa 10724  
Dbb 4583 cgcacagatgcgtaaggagaaaa 4605

RESULT 11

AAT13390

ID AAT13390 standard; DNA; 5323 BP.

XX

AC AAT13390;

XX

DT 24-JUN-1996 (first entry)

XX

DE Hybrid vector pSF1.

XX

KW Hybrid; vector; gene transfer; gene therapy; haematopoietic stem cell; retroviral; murine embryonic stem cell virus; MESV;

KW Moloney murine sarcoma virus; (MoMuSV);

KW Friend murine leukaemia virus; F-MuLV; ds.

XX

OS Synthetic.

XX

PN DE19503952-A1.

XX

PD 14-MAR-1996.

XX

PF 07-FEB-1995; 95DE-1003952.

XX

PR 08-SEP-1994; 94DE-1431973.



Qy	10402	cgcgcacattccccgaaaagtgccacctgacctgaagaaaccattattatcatgacat	10461
Db	4989		
		cgcgcacattccccgaaaagtgccacctgacctgaagaaaccattattatcatgacat	5048
Qy	10462	ttaacctataaaaaataggcgtatacgagggcccttttcgtctcgcgcgttccggtgatgacg	10521
Db	5049		
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Qy	10522	gtgaaaacctctgacacatgcaggtcccggagacgggtcacagcttgtgtgaagcggatg	10581
Db	5109		
		gtgaaaacctctgacacatgcaggtcccggagacgggtcacagcttgtgtgtgaagcggatg	5168
Qy	10582	ccgggagcagacaagcccgctcaggcgcgctcagcgggtgttgccgggtgtcgggctggc	10641
Db	5169		
		ccgggagcagacaagcccgctcaggcgcgctcagcgggtgttgccgggtgtcgggctggc	5228
Qy	10642	ttaactatgcggcatcagagcagattgtactgagagtgcaaccatatgcgggtgtgaaatac	10701
Db	5229		
		ttaactatgcggcatcagagcagattgtactgagagtgcaaccatatgcgggtgtgaaatac	5288
Qy	10702	cgcaccgaatcgcgcggaactaa	10724
Db	5289		
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RESULT 12
AAT13393
ID AAT13393 standard; DNA; 5364 BP.
XX
AC AAT13393;
XX
DT 24-JUN-1996 (first entry)
XX
DE Hybrid vector pMML.
XX
KW Hybrid; vector; gene transfer; gene therapy; haematopoietic stem cell;
KW retroviral; murine embryonic stem cell virus; MESV;
KW Moloney murine sarcoma virus; (MoMuSV);
KW Friend murine leukaemia virus; F-MuLV; ds.
KW

```

New hybrid vectors comprise (1) a leader region including the U5 region and tRNA primer binding site of murine embryonic stem cell virus (MESV) or Moloney murine sarcoma virus (MoMuSV), and (2) a 3'-LTR including the U3 and R regions of a Friend murine leukaemia virus (F-MuLV). The vectors are useful for ex-vivo or in-vivo gene therapy. High levels of gene transfer can be achieved in haematopoietic stem cells and their myeloid (non-lymphatic) progeny. pSF1, pSF2, pSF3 and pMM1 (sequences given in AAT13390-T13393) are examples of such vectors.

vector pSF-MDR (sequence given in AAT13394) is based on the MESV vector R224.



Db 4250 agccagccggaaggccgagcgagaaagtgttcctgcaactttatccgcctccatccagt 4309  
QY 9682 ctattaatgttgcgcgggaagctagagtaaagttagttccgccaagttaatagttttgcgaacg 9741  
Db 4310 ctattaatgttgcgcgggaagctagagtaaagttagttccgccaagttaatagtttgcgcaacg 4369  
QY 9742 ttgttgccattgtctacaggaatcgttggtgtcaagctcgtcgctgttgggtatggtcttcattca 9801  
Db 4370 ttgttgccattgtctacaggaatcgttggtgtcaagctcgtcgctgttgggtatggtcttcattca 4429  
QY 9802 gctccggttcccaacgatacaaggcgagttacatgatcccccatgttgtgcaaaaaagcgg 9861  
Db 4430 gctccggttcccaacgatacaaggcgagttacatgatcccccatgttgtgcaaaaaagcgg 4489  
QY 9862 ttagctccttcggtcctccgatcgttgttcagaagtaagtggccgcagtggttatcaactca 9921  
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QY 9922 tggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgctttctg 9981  
Db 4550 tggttatggcagcactgcataattctcttactgtcatgccatccgtaagatgctttctg 4609  
QY 9982 tgactggtgagtactcaaccaagtcattctgagaatagttgtatgcggcagccgagttgct 10041  
Db 4610 tgactggtgagtactcaaccaagtcattctgagaatagttgtatgcggcagccgagttgct 4669  
QY 10042 cttgcccggtcgaacacgggataataaccgcccacatagcagaactttaaaagtgtca 10101  
Db 4670 cttgcccggtcgaacacgggataataaccgcccacatagcagaactttaaaagtgtca 4729  
QY 10102 tcattgaaaaacgttcttcggggcgaaaaactcaaggatcttaccgctgttgagatcca 10161  
Db 4730 tcattgaaaaacgttcttcggggcgaaaaactcaaggatcttaccgctgttgagatcca 4789  
QY 10162 gttcgatgtaacccactcgtgcacccaactgatcttcagcatctttactttcaccagcg 10221  
Db 4790 gttcgatgtaacccactcgtgcacccaactgatcttcagcatctttactttcaccagcg 4849  
QY 10222 tttctgggtgagcaaaaaacagggaagcgcaaaatgccgcaaaaaagggaataaggcgacac 10281  
Db 4850 tttctgggtgagcaaaaaacagggaagcgcaaaatgccgcaaaaaagggaataaggcgacac 4909  
QY 10282 ggaatgtgaatactcatactctcttccttttccaattattattgaagcatttatcagggtt 10341  
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QY 10342 attgtctcatgagcggatacatatttgaatgtatttagaaaaataaaacaaatagggttc 10401  
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QY 10462 taacctataaaaaataggcgttatcacgagggcccttctcgtcgcggttccggtgatgacg 10521  
Db 5090 taacctataaaaaataggcgttatcacgagggcccttctcgtcgcggttccggtgatgacg 5149  
QY 10522 gtgaaaaacctctgacacatgcagctcccgagacggttcacagcttgtctgtgaagcggtatg 10581  
Db 5150 gtgaaaaacctctgacacatgcagctcccgagacggttcacagcttgtctgtgaagcggtatg 5209  
QY 10582 ccgggagcagacaagcccgctcaggggcgctcaggcggtgttggcggtgtcggggtggc 10641  
Db 5210 ccgggagcagacaagcccgctcaggggcgctcaggcggtgttggcggtgtcggggtggc 5269  
QY 10642 ttaactatcgggcatcagagcagattgttactgagagtgacaccatgcggtgtgaaatac 10701  
Db 5270 ttaactatcgggcatcagagcagattgttactgagagtgacaccatgcggtgtgaaatac 5329  
QY 10702 cgcaccgaatcgcgcggaactaa 10724  
||||| || || ||| ||

Db 5330 cgcacagatcgctaaggagaaaa 5352  
RESULT 13  
AAC60706  
ID AAC60706 standard; DNA; 5374 BP.  
XX  
AC AAC60706;  
XX  
DT 30-JAN-2001 (first entry)  
XX  
DE Primers attached vector elongation method vector pED6pdc2.  
XX  
KW Primers attached vector elongation; PAVE; plasmid vector;  
KW cDNA library construction; ds.  
XX  
OS Synthetic.  
XX  
PN WO200056913-A1.  
XX  
PD 28-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US07332.  
XX  
PR 19-MAR-1999; 99US-0125596.  
XX  
PA (GEMY ) GENETICS INST INC.  
XX  
PI Song C, Brown JC, Leeying W, Rivera DS;  
XX  
DR WPI; 2000-638266/61.  
XX  
PT Preparing modified a mRNA molecule for constructing a cDNA library  
PT comprises ligating a tag which consists of ribonucleotide residues and  
PT does not have any deoxyribonucleotide residues, to the 5' end of an  
PT mRNA molecule -  
XX  
PS Disclosure; Fig 6; 65pp; English.  
XX  
CC The present invention is concerned with a novel method for cDNA library  
CC construction. This involves the use of tagged sample mRNA molecules for  
CC amplification using primers contained within vectors. The RNA is then  
CC digested, second strand synthesis is performed and the resulting molecule  
CC comprises a vector containing the desired cDNA sequence. The present  
CC sequence is a vector used to demonstrate the method. The method can be  
CC used as a more efficient and reliable way of obtaining full-length cDNA  
CC libraries. The method is known as primers attached vector  
XX  
SQ Sequence 5374 BP; 1320 A; 1337 C; 1399 G; 1318 T; 0 other;  
Query Match 18.2%; Score 2034.2; DB 21; Length 5374;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 8662 agttcaagaagaaggcggtttttccataggtctccgccccctgacgagcatcacaaaaatc 8721  
Db 3138 aggcgcggttgctggcggtttttccataggtctccgccccctgacgagcatcacaaaaatc 3197  
QY 8722 gacgctcaagtcagaggtggcgaaaccccgacaggactataaagataccaggcgtttcccc 8781  
Db 3198 gacgctcaagtcagaggtggcgaaaccccgacaggactataaagataccaggcgtttcccc 3257  
QY 8782 ctggaagctccctcgtgcgctctctctgttcccgacctgcgcttaccggataacctgtccg 8841  
Db 3258 ctggaagctccctcgtgcgctctctctgttcccgacctgcgcttaccggataacctgtccg 3317  
QY 8842 cctttctcccttcgggaagcgtggcgcttttctcaatgctcagcgtgtaggtatctcagtt 8901  
Db 3318 cctttctcccttcgggaagcgtggcgcttttctcaatgctcagcgtgtaggtatctcagtt 3377  
QY 8902 cgggtgtaggtcgttcgctccaagctggggtgtgtgcacgaaccccccgcttcacgcccgacc 8961

Db 3378 ||||| cggtaggtcgctccaaagctgggtgtgtgcacgaaccccggttcagcccgacc 3437

Qy 8962 gctgcgccttatccggtaaactatcgtcttgagtgccaacccggtgaagacacgacttatcgc 9021

Db 3438 gctgcgccttatccggtaaactatcgtcttgagtgccaacccggtgaagacacgacttatcgc 3497

Qy 9022 cactggcagcagccactggtaaacaggattagcagagcgaggtatgtaggcgtgctacag 9081

Db 3498 cactggcagcagccactggtaaacaggattagcagagcgaggtatgtaggcgtgctacag 3557

Qy 9082 agttctttgaagtggcgccctaactacggtacactagaaggacagttattggatatctgcg 9141

Db 3558 agttctttgaagtggcgccctaactacggtacactagaaggacagttattggatatctgcg 3617

Qy 9142 ctctgctgaagccagttaccttcctcgaaaaagagttggtagctcttgatccggcaaacaaa 9201

Db 3618 ctctgctgaagccagttaccttcctcgaaaaagagttggtagctcttgatccggcaaacaaa 3677

Qy 9202 ccaccgctgtagcgtggtttttttgtttgcaagcagcagattacgcgcagaaaaaaaag 9261

Db 3678 ccaccgctgtagcgtggtttttttgtttgcaagcagcagattacgcgcagaaaaaaaag 3737

Qy 9262 gatctcaagaagatccctttgatcttttctacggggtctgacgctcagtggaacgaaaaact 9321

Db 3738 gatctcaagaagatccctttgatcttttctacggggtctgacgctcagtggaacgaaaaact 3797

Qy 9322 cactgtaagggatttttggtcatgagattatcaaaaaggatcttccactagatcccttttaa 9381

Db 3798 cactgtaagggatttttggtcatgagattatcaaaaaggatcttccactagatcccttttaa 3857

Qy 9382 attaaaaatgaagtttttaaatcaatctaaagtatatatgagtaaaacttggctcgacagtt 9441

Db 3858 attaaaaatgaagtttttaaatcaatctaaagtatatatgagtaaaacttggctcgacagtt 3917

Qy 9442 accaatgcttaataatcagtgaggcaacctatctcgaagatctgtctatttctgctccatccatag 9501

Db 3918 accaatgcttaataatcagtgaggcaacctatctcgaagatctgtctatttctgctccatccatag 3977

Qy 9502 ttgcctgactccccgtcgtgtagataaactacgatacgggaggttaccatctggcccca 9561

Db 3978 ttgcctgactccccgtcgtgtagataaactacgatacgggaggttaccatctggcccca 4037

Qy 9562 gtgctgcaatgataccgcgagacccacgctcacccgctccagattttatcagcaataaaacc 9621

Db 4038 gtgctgcaatgataccgcgagacccacgctcacccgctccagattttatcagcaataaaacc 4097

Qy 9622 agccagccggaaaggccgagcgagaaagtgtcctgcaactttatccgcctccatccagtt 9681

Db 4098 agccagccggaaaggccgagcgagaaagtgtcctgcaactttatccgcctccatccagtt 4157

Qy 9682 ctattaaattgtgcccgggaagctagagtaagtagttgccaggttaatagttttgcgcaacg 9741

Db 4158 ctattaaattgtgcccgggaagctagagtaagtagttgccaggttaatagttttgcgcaacg 4217

Qy 9742 ttggtgccattgctacagggcatcgtgggtgcacgctcgtcgttttggtatggcttcattca 9801

Db 4218 ttggtgccattgctacagggcatcgtgggtgcacgctcgtcgttttggtatggcttcattca 4277

Qy 9802 gctccgggttcccaacgatcaaggcgaggttacatgatcccccatgttgtgcaaaaaaagcgg 9861

Db 4278 gctccgggttcccaacgatcaaggcgaggttacatgatcccccatgttgtgcaaaaaaagcgg 4337

Qy 9862 ttagctccttcggctcctccgatcgtttgtcagaagaagtaagttggccgcaggtttatcaactca 9921

Db 4338 ttagctccttcggctcctccgatcgtttgtcagaagaagtaagttggccgcaggtttatcaactca 4397

Qy 9922 tgggtatggcagcactgcataattctcttactgtcatgccatcccgtaagatgcttttctg 9981

Db 4398 tgggtatggcagcactgcataattctcttactgtcatgccatcccgtaagatgcttttctg 4457

Qy 9982 tgacttggtgagtactcaaccaagtcatcttgagaatagtgtatcggcgacccgagttgct 10041

Db 4458 tgactgggtgagtactcaaccaagtcatctctgagaatagtgtagcggcgacccgagttgct 4517

Qy 10042 cttgccccgcgtcaacacgaggdataataaccgcgcacacatagcagaaactttaaaaagtgtca 10101

Db 4518 cttgccccgcgtcaatacagggataataaccgcgcacacatagcagaaactttaaaaagtgtca 4577

Qy 10102 tcaattggaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 10161

Db 4578 tcaattggaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 4637

Qy 10162 gttcgatgtaacccactcgtgcaccccaactgatcttcagcatcttttacttttaccagcg 10221

Db 4638 gttcgatgtaacccactcgtgcaccccaactgatcttcagcatcttttacttttaccagcg 4697

Qy 10222 tttctgggtgagcaaaaaacagggaaggcaaaatccgcaaaaaagggaataaaggcgacac 10281

Db 4698 tttctgggtgagcaaaaaacagggaaggcaaaatccgcaaaaaagggaataaaggcgacac 4757

Qy 10282 ggaaatgttgaatactcatactactcttctcttcttcttcaatatatttgaagcatttatcagggtt 10341

Db 4758 ggaaatgttgaatactcatactactcttctcttcttcttcaatatatttgaagcatttatcagggtt 4817

Qy 10342 attgtctcatgagcgggatacatatttgaatgtatttagaaaaataaacaataaggggttc 10401

Db 4818 attgtctcatgagcgggatacatatttgaatgtatttagaaaaataaacaataaggggttc 4877

Qy 10402 cgcgcacatttccccgaaaaagtgccacctgacgtctaaagaaaccattattatcatgacat 10461

Db 4878 cgcgcacatttccccgaaaaagtgccacctgacgtctaaagaaaccattattatcatgacat 4937

Qy 10462 taacctataaaaaataggcgtatcaagaggccctttctcgtcgcgcgttttcggtgatgacg 10521

Db 4938 taacctataaaaaataggcgtatcaagaggccctttctcgtcgcgcgttttcggtgatgacg 4997

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Qy 10582 ccgggagcagacaaagcccgtcagggcgctcagcgggtgttggcgggtgtcggggtggc 10641

Db 5058 ccgggagcagacaaagcccgtcagggcgctcagcgggtgttggcgggtgtcggggtggc 5117

Qy 10642 ttaactatcgggcatcagagcagattgtactgagagtgcaccatatgcggtgtgaaaatac 10701

Db 5118 ttaactatcgggcatcagagcagattgtactgagagtgcaccatatgcggtgtgaaaatac 5177

Qy 10702 cgcaccggaatcgcgcggaactaa 10724

Db 5178 cgcacagatgcgtaaggagaaaa 5200

RESULT 14

AAC68299

ID AAC68299 standard; DNA; 5421 BP.

XX

AC AAC68299;

XX

DT 20-FEB-2001 (first entry)

XX

DE SV40/APPA plasmid coding sequence.

XX

KW Transgenic animal; salivary protein; phytase; phosphorus; animal growth; environmental pollution; pig; ds.

XX

OS Rhesus macaque polyoma virus - chimeric.

OS Escherichia coli - chimeric.

XX

PN W0200064247-A1.

XX

PD 02-NOV-2000.

XX

PF 20-APR-2000; 2000WO-CA00430.

XX

PR 23-APR-1999; 99US-0130508.  
XX (UYGU-) UNIV GUELPH.  
PA Forsberg CW, Golovan S, Phillips JP;  
XX WPI; 2000-687245/67.  
DR P-PSDB; AAB36262.  
XX Transgenic non-human animal for gastrointestinal tract specific  
PT expression of a protein, preferably phytase, comprises a nucleic acid  
PT sequence including a heterologous transgene construct encoding the  
PT protein -  
XX Claim 56; Fig 22; 152pp; English.  
PS The present invention provides transgenic animals which produce desired  
XX proteins, in this case pigs which expresses phytase in the salivary  
CC gland. Low phytase production levels result in phytate in the diet being  
CC excreted and causing phosphorus contamination in water, as well as  
CC reducing the growth of animals. The invention provides a number of  
CC transgenes containing the E. coli APPA phytase coding sequence.  
XX Sequence 5421 BP; 1413 A; 1321 C; 1331 G; 1355 T; 1 other;  
SQ

Query Match 18.2%; Score 2034.2; DB 21; Length 5421;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2045; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 8662 agttcaagaagaaggcgtttttccataggctccgccccctgacgagcatcacaaaaac 8721  
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Db 2687 aggccgcgttgctggcgtttttccataggctccgccccctgacgagcatcacaaaaac 2746

QY 8722 gacgctcaagtcagaggtggcgaaaccgacagagactataaagataccaggcgtttcccc 8781  
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 2747 gacgctcaagtcagaggtggcgaaaccgacagagactataaagataccaggcgtttcccc 2806

QY 8782 ctggaagctccctcgtgcgtctctctgttcgcacccctgcgcttacccgataccgtgccg 8841  
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Db 2807 ctggaagctccctcgtgcgtctctctgttcgcacccctgcgcttacccgataccgtgccg 2866

QY 8842 cctttctccctcgggaagcgtggcgctttctcaatgctcacgctgtaggtatctcagtt 8901  
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 2867 cctttctccctcgggaagcgtggcgctttctcaatgctcacgctgtaggtatctcagtt 2926

QY 8902 cgggtgtagctcgtctccaagctgggctgtgtgcacgaaccccccttcagccgacc 8961  
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Db 2927 cgggtgtagctcgtctccaagctgggctgtgtgcacgaaccccccttcagccgacc 2986

QY 8962 gctgcgccttatccggtaactatcgtcttgagtcctcaaccccggtgaacacgacttatcgc 9021  
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 2987 gctgcgccttatccggtaactatcgtcttgagtcctcaaccccggtgaacacgacttatcgc 3046

QY 9022 cactggcagcagccactggttaacaggattagcagagcgaggtatgtaggcgggtgctacag 9081  
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Db 3047 cactggcagcagccactggttaacaggattagcagagcgaggtatgtaggcgggtgctacag 3106

QY 9082 agttctgaagtggtggcctaactacggtacactagaaggacagtatttggtatctgcg 9141  
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Db 3107 agttctgaagtggtggcctaactacggtacactagaaggacagtatttggtatctgcg 3166

QY 9142 ctctgtgaagccagttacccttcggaaaaagagttggtagctcttgatcccgcaaaacaa 9201  
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Db 3167 ctctgtgaagccagttacccttcggaaaaagagttggtagctcttgatcccgcaaaacaa 3226

QY 9202 ccaccgctggtgagcgggtgtttttttgttgcaagcagcagattacgcgcagaaaaaaaag 9261  
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Db 3227 ccaccgctggtgagcgggtgtttttttgttgcaagcagcagattacgcgcagaaaaaaaag 3286

QY 9262 gatctcaagaagatcctttgatcttttctacggggtctgacgctcagtggaacgaaaaact 9321  
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Db 3287 gatctcaagaagatcctttgatcttttctacggggtctgacgctcagtggaacgaaaaact 3346

QY 9322 cacgttaagggttttggatgagattatcaaaaaaggatcttcacctagatccttttaa 9381  
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Db 3347 cacgttaagggttttggatgagattatcaaaaaaggatcttcacctagatccttttaa 3406

QY 9382 attaaaaatgaagtttttaaatcaatctaaaagtatatatgagtaaaacttggtctgacagtt 9441  
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Db 3407 attaaaaatgaagtttttaaatcaatctaaaagtatatatgagtaaaacttggtctgacagtt 3466

QY 9442 accaatgcttaatcagtgaggcacctatctcagcgatctgtctatttcgttccatccatag 9501  
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Db 3467 accaatgcttaatcagtgaggcacctatctcagcgatctgtctatttcgttccatccatag 3526

QY 9502 ttgcctgactcccccgctcgtgtagataaactacgatacgggagggcttaccatctggcccca 9561  
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QY 9562 gtgctgcaatgataccgagagaccacgctcaccggctccagatttatcagcaataaaacc 9621  
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Db 3587 gtgctgcaatgataccgagagaccacgctcaccggctccagatttatcagcaataaaacc 3646

QY 9622 agccagccggaaggccgagcgagagaagtgtctcgaactttatccgcctccatccagt 9681  
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Db 3647 agccagccggaaggccgagcgagagaagtgtctcgaactttatccgcctccatccagt 3706

QY 9682 ctattaaattgttgcgggaagctagagtaaagttagtgccaggttaataagtttgcgcaacg 9741  
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Db 3707 ctattaaattgttgcgggaagctagagtaaagttagtgccaggttaataagtttgcgcaacg 3766

QY 9742 ttgttgccattgctacagggcatcgtggtgtcagcgtcgtcgtttggtatggcttcattca 9801  
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Db 3767 ttgttgccattgctacagggcatcgtggtgtcacgctcgtcgtttggtatggcttcattca 3826

QY 9802 gctccggttcccaacgatcaaggcgaggttacatgatcccccatgttgtgcataaaagcgg 9861  
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Db 3827 gctccggttcccaacgatcaaggcgaggttacatgatcccccatgttgtgcataaaagcgg 3886

QY 9862 ttagctccttcggtcctccgatcgttgttcagaagtaagtggccgcagtggttatcactca 9921  
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Db 3887 ttagctccttcggtcctccgatcgttgttcagaagtaagtggccgcagtggttatcactca 3946

QY 9922 tggttatggcagcactgcataaattctcttactgtcatgccatccgtaagatgcttttctg 9981  
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Db 3947 tggttatggcagcactgcataaattctcttactgtcatgccatccgtaagatgcttttctg 4006

QY 9982 tgactggtgagtactcaaccaaagtcattcttgagaataagtgtatgcggcgacgagttgct 10041  
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 4007 tgactggtgagtactcaaccaaagtcattcttgagaataagtgtatgcggcgacgagttgct 4066

QY 10042 cttgccccgctcaacacagggataataacccgcccacatagcagaactttaaaagtgtca 10101  
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Db 4067 cttgccccgctcaacacagggataataacccgcccacatagcagaactttaaaagtgtca 4126

QY 10102 tcattggaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 10161  
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Db 4127 tcattggaaaaacgttcttcggggcgaaaaactctcaaggatcttaccgctgttgagatcca 4186

QY 10162 gttcgtgtaacccactcgtgcacccaactgatcttcagcatcttttactttcaccagcg 10221  
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Db 4187 gttcgtgtaacccactcgtgcacccaactgatcttcagcatcttttactttcaccagcg 4246

QY 10222 tttctgggtgagcaaaaaacagggaagcaaaatcccgcaaaaaagggaataagggcgacac 10281  
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 4247 tttctgggtgagcaaaaaacagggaagcaaaatcccgcaaaaaagggaataagggcgacac 4306

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 22:09:21 ; Search time 19406.3 Seconds  
(without alignments)  
12083.829 Million cell updates/sec

Title: US-09-700-843-1  
Perfect score: 11206  
Sequence: 1 catgatgaaataacataagg.....cacgatgagaatgccagac 11206

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
  
Searched: 1797656 seqs, 10463268293 residues  
  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

1	11206	100.0	11206	6	E30143	E30143 Vector for
2	11195	99.9	11207	3	AB028139	AB028139 Drosophil
3	5433.2	48.5	8780	12	PEU59056	U59056 P element t
4	5433.2	48.5	9255	12	PEU60735	U60735 P element t
5	5096.2	45.5	12294	12	DMCASPLC2	X81643 D.melanogas
6	5055.4	45.1	10020	12	AF242362	AF242362 Green pel
7	5055.4	45.1	10095	12	AF242364	AF242364 Stinger G
8	5055.4	45.1	10189	12	AF242363	AF242363 Green H-P
9	5055.4	45.1	10288	12	AF242365	AF242365 H-Stinger
10	5055.4	45.1	13336	12	AF242360	AF242360 Pelican l
11	5055.4	45.1	13508	12	AF242361	AF242361 H-Pelican
12	5044	45.0	7862	12	DMCASPER4	X81645 D.melanogas
13	5042.6	45.0	7815	12	PEU59054	U59054 P element t
14	5042	45.0	7775	12	DMCASPER1	X81644 D.melanogas
15	5041.6	45.0	7815	12	PEU59055	U59055 P element t
16	2891.8	25.8	3271	8	SCYPL248C	Z73604 S.cerevisia
17	2891.8	25.8	3694	8	YSCGAL4	K01486 Yeast (S.ce
18	2891.8	25.8	37808	8	SC38KCXVI	Z67751 S.cerevisia
19	2760	24.6	3616	12	SYNNEGIE	M30841 Vector cont
20	2628.4	23.5	2646	6	E06922	E06922 DNA encodin
21	2538.2	22.7	14245	3	DMWHITE	X02974 Drosophila
22	2439.6	21.8	7485	2	AC013055	AC013055 Drosophil
23	2439.6	21.8	45752	3	DMBN33B1	AL133506 Drosophil
24	2439.6	21.8	162436	2	AC104145	AC104145 Drosophil
25	2439.6	21.8	300205	3	AE003425	AE003425 Drosophil
26	2143.2	19.1	8932	12	U03463	U03463 Cloning vec
27	2108.8	18.8	5805	3	DSU64875	U64875 Drosophila
28	2103	18.8	9386	12	U03462	U03462 Cloning vec
29	2102.8	18.8	7286	6	AR112486	AR112486 Sequence
30	2102.8	18.8	7286	6	E34421	E34421 Inductive p
31	2034.2	18.2	2905	12	SYNPKP497A	M74187 Cloning vec
32	2034.2	18.2	3024	1	PK9CCDB	L27082 Plasmid KIL
33	2034.2	18.2	3024	12	SYNCCDBC	L38497 Cloning vec
34	2034.2	18.2	3582	12	SYNECOMCS	M68946 Cloning vec
35	2034.2	18.2	3642	12	SYN260BLA	M29362 Plasmid pFL
36	2034.2	18.2	3875	6	AR147724	AR147724 Sequence
37	2034.2	18.2	3875	6	AR159746	AR159746 Sequence
38	2034.2	18.2	3875	6	AR160438	AR160438 Sequence
39	2034.2	18.2	3878	6	AR147730	AR147730 Sequence
40	2034.2	18.2	3878	6	AR159752	AR159752 Sequence
41	2034.2	18.2	3878	6	AR160444	AR160444 Sequence
42	2034.2	18.2	3883	6	AR147733	AR147733 Sequence
43	2034.2	18.2	3883	6	AR159755	AR159755 Sequence
44	2034.2	18.2	3883	6	AR160447	AR160447 Sequence
45	2034.2	18.2	3908	6	AR147727	AR147727 Sequence

ALIGNMENTS

RESULT	1					
E30143		E30143	11206 bp	DNA	linear	PAT 07-FEB-2001
LOCUS		Vector for gene trapping and method for gene trapping by using said				
DEFINITION		vector.				
ACCESSION		E30143				
VERSION		E30143.1	GI:13016987			
KEYWORDS		JP 1999332564 -A/1.				
SOURCE		unidentified.				
ORGANISM		unidentified				
		unclassified.				
REFERENCE		1 (bases 1 to 11206)				
AUTHORS		Rukachobitchi,T.A.Z.Z. and Yamamoto,W.A.				
TITLE		Vector for gene trapping and method for gene trapping by using said				
JOURNAL		vector				
		Patent: JP 1999332564-A 1 07-DEC-1999;				
		SCIENCE & TECH AGENCY				
COMMENT		OS Unidentified				
		PN JP 1999332564 -A/1				
		PD 07-DEC-1999				
		PF 22-MAY-1998 JP 1998141952				
		PR				
		PI RUKACHOBITCHI TAMASSHU,ASUTAROSSHU ZORUDAN,DAISUKE YAMAMOTO,				



PI		WAKAE AWANO	
PC		C12N15/09//((C12N15/09,C12R1:91),C12N15/00,(C12N15/00,C12R1:91))	
CC		Strandedness: Double;	
CC		Topology: Circular;	
FH		Key	Location/Qualifiers
FT		source	1. .11206
FT			/organism='Unidentified'.
FEATURES			
source		1. .11206	
		/organism="unidentified"	
		/db_xref="taxon:32644"	
BASE COUNT		2998 a	2648 c 2564 g 2996 t
ORIGIN			
Query Match 100.0%; Score 11206; DB 6; Length 11206;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 11206; Conservative 0; Mismatches 0; Indels 0; Gaps 0.			
QY	1	catgatgaaataacataaagtggtcccgctcggcaagagacatccacttaacgtatgcttg	60
Db	1	CATGATGAATAACATAAAGTGGTCCCGTCGGCAAGAGACATCCACTTAACGTATGCTTG	60
QY	61	caataagtcgagtgaaaggaatagttattcttgagtgctgattgagtcgagtgagacag	120
Db	61	CAATAAGTCGAGTGAAGGAATAGTATTCTGAGTGTCTGATTGAGTCTGAGTGAGACAG	120
QY	121	cgatatgattgttgattaaaccccttagcatgtccgtggggttgaaattaactcataatatt	180
Db	121	CGATATGATTGTTGATTAAACCCTTAGCATGTCCGTGGGGTTTGAATTAACTCATAATATT	180
QY	181	aattagacgaaattatttttaaagttttatttttaataaatttcgagtagcgaagctct	240
Db	181	AATTAGACGAAATTATTTTAAAGTTTATTATTTTAATAATTTCGAGTACGCAAAAGCTCT	240
QY	241	ttctctacaggtcgaattgatgtgatggatcccaatgaagctactgtcttctatogaaca	300
Db	241	TTCTCTTACAGGTCGAATTGATGTGATGGATCCCAATGAAGCTACTGTCTTCTATCGAACA	300
QY	301	agcatgcgatatttgcgacttaaaaaagctcaagtgtctccaaagaaaaacccaagtgccg	360
Db	301	AGCATGCGGATATTGCCGACTTAAAAAGCTCAAGTGTCTCCAAAGAAAAACCGAAGTGCGC	360
QY	361	caagtgtctgaagaacaaactgggagtgctgcgtactctcccaaaaccaaaggctccgct	420
Db	361	CAAGTGTCTGAAGAACAACTGGGAGTGTGCTACTCTCCCAAAACCAAAGTCTCCGCT	420
QY	421	gactagggcacatctgacagaagtggaatcaaggctagaaagactggaaacagctatttct	480
Db	421	GACTAGGGCACATCTGACAGAAGTGGAATCAAGGCTAGAAAGACTGGAACAGCTATTCT	480
QY	481	actgatttttctctcgagaagaccttgacatgattttgaaaaatggattctttacaggatat	540
Db	481	ACTGATTTTTCCTCGAGAAGACCTTGACATGATTTTGAAAATGGATTCTTTACAGGATAT	540
QY	541	aaaagcattgttaacaggattattttgtacaagataaatgtgaataaaagatccgtcacaga	600
Db	541	AAAAGCATTGTTAACAGGATTATTGTACAAGATAAATGTGAATAAAGATGCCGTACAGA	600
QY	601	tagattggcttcagtgagactgatatgcctctaacattgagacagcatagaataaagtcg	660
Db	601	TAGATTGGCTTCAGTGGAGACTGATATGCCTCTAACATTGAGACAGCATAGAAATAAGTGC	660
QY	661	gacatcatcatcggaaagagagtagtagtaacaaaaggtcgaagacacagttgactgtatcgattga	720
Db	661	GACATCATCATCGGAAGAGAGTAGTAACAAAGGTCAAAAGACAGTTGACTGTATCGATTGA	720
QY	721	ctcggcagctcatcatgataactcccaaatctccgttggtgattttatgccagggatgctct	780
Db	721	CTCGGCAGCTCATCATGATAACTCCACAATTCGGTGGATTTTATGCCAGGGATGCTCT	780
QY	781	tcattgattgattggtctgaagaggatgacatgtcggatggcttgcccttcctgaaac	840
Db			

Db	781	TCATGGATTTGATTGGTCTGAAGAGGATGACATGTCGGATGGCTTGCCCTTCTTGAAAAAC	840
QY	841	ggacccccacaataatgggttctcttggcgaggttctctcttattgtattcttcgatctat	900
Db	841	GGACCCCAACAATAATGGGTCTTTTGGCGAGGTTCTCTCTTATGTATTCTTCGATCTAT	900
QY	901	tggtctttaaacccggaaaaattacacgaaacttaacggttaacaggtcccgaccatgattac	960
Db	901	TGGCTTTAAACCCGGAAAAATTACACGAACCTAACGTTAACAGGCTCCGACCATGATTAC	960
QY	961	ggatagatacacgttggtcttcttagatccacaacatcccgtttacttcaaaagtattctcaa	1020
Db	961	GGATAGATACACGTTGGCTTCTAGATCCACAACATCCCGTTTACTTCAAAAGTTATCTCAA	1020
QY	1021	taattttcacccctactgccctatcgtgcactcacgcgactaatgatgtgtataataa	1080
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QY	1081	ccagattgaaatcgctggaaggatcaatggcaaatcctttttaactgcataattagccat	1140
Db	1081	CCAGATTGAAATCGCGTCGAAGGATCAATGGCAAAATCCTTTTAACTGCATATTAGCCAT	1140
QY	1141	tggagcctgggtatagagggggaatctactgatatagatgttttttactatcaaaaatgc	1200
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QY	1201	taaatctcatttgacgagcaaggtcttcgagtcaggttccataaattttggtgacagccct	1260
Db	1201	TAAATCTCAITTGACGAGCAAGGCTCTCGAGTCAGGTTCCATAAATTTGGTGACAGCCCT	1260
QY	1261	acatcttctgcgcgatatacacacagtgaggcgagaaaaaataactagctataaatttca	1320
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QY	1321	cagcttttccataaagaatggccataatactgggttgaaataggagacctcccctcgtcctt	1380
Db	1321	CAGCTTTTCCATAAGAATGGCCATATCATTTGGGCTTGAATAGGACCTCCCCCTCGTCTT	1380
QY	1381	cagttagcagcattcttgaaacaaagacgccgaatttgggtgctgtctgtactcttggga	1440
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QY	1621	aactgcagaaaaaagtccctatatgtgcaaaaaaaatgcttgatgatttghtaatgagattga	1680
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QY	1741	caatttgttgaaaggaacaccccttggtctatccctttacaagattcgaactgaagtgaataaca	1800
Db	1741	CAATTTGTTGAAGGAACACCCCTTGCTATCCTTTACAAGATTCGAACTGAAGTGGAAACA	1800
QY	1801	gttgtcttattcatcttattgtattaagagattttttcactaattttaccagaaaaagtc	1860
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ORGANISM	Drosophila melanogaster
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AUTHORS	1 (sites) Lukacsovich,T., Asztalos,Z., Awano,W., Baba,K., Kondo,S., Niwa,S. and Yamamoto,D.
TITLE	Dual-Tagging Gene Trap of Novel Genes in Drosophila melanogaster
JOURNAL	Genetics 157 (2), 727-742 (2001)
PUBMED	11156992
REFERENCE	2 (bases 1 to 11207)
AUTHORS	Lukacsovich,T.
TITLE	Direct Submission
JOURNAL	Submitted (31-MAY-1999) Tamas Lukacsovich, Mitsubishi Kasei Inst. of Life Sci., ERATO, JST, Yamamoto Behavior Genes Project; 11 Minamiooya, Machida, Tokyo 194, Japan
FEATURES	(E-mail:lukacs@fly.erato.jst.go.jp, Tel.:81-427-212334, Fax:81-427-212850)
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ORIGIN	

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QY 3181 aaagccaaatagaaaattattcagttcttggttaagtttttaaaagtgatattattttt 3240  
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[illegible]

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Db	5641	CTCGCTATATAAGACAAATTTTAAGATCATATCATGATCAAGACATCTAAAGGCATTCA	5700
QY	5701	ttttcgactacattcttttttacaaaaataataacaaccagatatatttaagctgaccta	5760
Db	5701	TTTTTCGACTACATTCTTTTACAAAAATATAACAACCAGATATTTTAAGCTGATCCTA	5760
QY	5761	gatgcacaaaaataataaaaaagtataaacctactctcgtaggatacttctgtttcttcgg	5820
Db	5761	GATGCACAAAAATAAATAAAAGTATAAACCTACTTCGTAGGATACTTCGTTTGTTCGG	5820
QY	5821	ggttagatgagcataaacgcttgtagttgatatatttgagatccccctatcatgcagggtagc	5880
Db	5821	GGTTAGATGAGCATAAACGCTTGTAGTTGATATTGAGATCCCCATATCATTCAGGGTGAC	5880
QY	5881	agcggacgcttcgcagagctgcattaaaccagggttcgggcaggccaaaaactacggcac	5940
Db	5881	AGCGGACGCTTCGCAGAGCTGCATTAAACCAGSGCTTCGGGCAGGCCAAAAAACTACGGCAC	5940
QY	5941	gctcctgccaccagtcgcgcggaggactcgggttcagggagcggccaaactagccgagaa	6000
Db	5941	GCTCCTGCCACCCAGTCCGCCGGAGGACTCCGGTTCAGGGAGCGGCCAACTAGCCGAGAA	6000
QY	6001	cctcaacctatgcctggcacaaatatggacatctttggggcgggtcaatcagccgggctccgg	6060
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QY	6061	atggcggcagctggtcaaccggacacgcggactattctgcaacgagcgcacataccggc	6120
Db	6061	ATGGCGGCAGCTGGTCAACCCGACACCGCGACTATTCTGCAACGAGCGACACATACCGGC	6120
QY	6121	gccaggaaacatttgctcaagaacggtgagtttctatttcgacgtcggctgactgtgtg	6180
Db	6121	GCCCAGGAACATTGCTCAAGAACGGTGAGTTCTATTTCGCAGTCGGCTGATCTGTGTG	6180
QY	6181	aaatcttaataaagggtccaattaccaatttgaaactcagtttgcgcggtgacctatccg	6240
Db	6181	AAATCTTAATAAAGGTTCCAATTACCAAATTGAAAACTCAGTTTGGCGGTGACTATCCG	6240
QY	6241	ggcgaaacttttggccgtgatgggcagttccggtgcgggaaagacgacctgctgaatgcc	6300
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Db	6301	CTTGCCCTTCGATCGCCGACAGGCATCCAAAGTATCGCCATCCGGGATGCCGACTGCTCAAT	6360
QY	6361	ggccaaacctgtggacgccaaaggagatgcaggccaggtgcgcctatgtccagcaggatgac	6420
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Db	6421	CTCTTTATCGGCTCCCTAACGGCCAGGGAACACCTGATTTTCCAGGCCCATGCTGCGGATG	6480
QY	6481	ccacgacatctgacctatcggcagcgcagtgccgcgcgtggatcaggtgatccaggagcctt	6540
Db	6481	CCACGACATCTGACCTATCGGCAGCGAGTGGCCCGCGTGGATCAGGTGATCCAGGAGCTT	6540
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Db	6541	TCGCTCAGCAAAATGTCAGCACACCATCATCTCGGTGTGCCCCGGCAGGGTGAAAGTCTGTCC	6600
QY	6601	ggcggagaaaggaagcgtctggcattcgccctcggaggcactaaaccgatccgcgcctctgt	6660
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QY	6661	atctgcgatgagcccaacctccggactggactcaattaccgcccacagcgtcgtccagggtg	6720
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Db	8941	GAACCCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAAC	9000	
Qy	9000	ccggtaaagacacgacttatcgccactggcagcagccactggtaaacaggattagcagagcg	9059	
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Qy	9060	aggatatgtaggcggtgtacagagttcttgaagtgggtgcctaaactacggtacactaga	9119	
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Qy	9120	aggacagtatgtgtatctgcgtctctgtgaagccagttaccttcggaaaaagagttggt	9179	
Db	9121	AGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGT	9180	
Qy	9180	agctcttgatccgggaaacaaacaccgcgctggtagcgggtgtttttttgtttgcaagcag	9239	
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Qy	9240	cagattacgcgcagaaaaaaggatctcaagaagatcccttggatccttttcttacggggtct	9299	
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Qy	9300	gacgctcagtggaacgaaaaactcacggttaagggattttggtcatgagattatcaaaaaagg	9359	
Db	9301	GACGCTCAGTGGAACCAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGG	9360	
Qy	9360	atcttccacctagatccctttaaataaaatgaagttttaaatacaatcctaagtatatat	9419	
Db	9361	ATCTTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATAT	9420	
Qy	9420	gagttaaactgtgtgacaggttaccaaagcttaatacagtgaggcacctatctcagcgcac	9479	
Db	9421	GAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATC	9480	
Qy	9480	tgctatttcgttcacatcagttgcctgactccccgctcgtgtagataaactacgatacgg	9539	
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Qy	9540	gagggcttaccatctggccccagtgctgcaatgataccgcgagacccacgctcacccgct	9599	
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Qy	9600	ccagatttatcagcaataaaaccagccagccggaaggccgagcgcagaagtggctcctgca	9659	
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Qy	9660	actttatccgcctccatccagtcctattaatgttgccgggaagcgtagagtaagtagttcg	9719	
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Qy	9720	ccagttaatagtttgcgcaacggttggttgccattgctacaggcatcgttggtcacgcctcg	9779	
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Qy	9780	tcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttacatgatcc	9839	
Db	9781	TCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCTCAACGATCAAGGGCAGTTACATGATCC	9840	
Qy	9840	cccatggtgtgcaaaaaagcggttagctccctcgttcctccgatcgttgtcagaagtaag	9899	
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Qy	9900	ttggccgcagtggttatcactcatggttatggcagcactgcataattctcttactgtcatg	9959	
Db	9901	TTGGCCGCAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATG	9960	
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TITLE New pCaSpeR P element vectors  
JOURNAL Dros. Info. Service 71, 150-150 (1992)  
REFERENCE 2 (bases 1 to 8780)  
AUTHORS Thummel,C.S. and Pirrotta,V.  
TITLE Direct Submission  
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AUTHORS Thummel,C.S., Woodard,C.T. and Pirrotta,V.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUN-1996) Human Genetics, University of Utah, 5200  
Eccles Institute, Bldg. 533, Salt Lake City, UT 84112, USA  
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AUTHORS Pirrotta,V. and Zeng,C.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 12294)  
AUTHORS Pirrotta,V.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-1994) V. Pirrotta, Dept of Zoology, University of  
Geneva, 30 Quai E. Ansermet, 1211 Geneva, SWITZERLAND  
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VERSION AF242362.2 GI:12237296  
KEYWORDS  
SOURCE Green Pelican GFP transformation vector.  
ORGANISM Green Pelican GFP transformation vector  
artificial sequence; vectors.  
REFERENCE 1 (bases 1 to 10020)  
AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.  
TITLE GFP and beta-galactosidase transformation vectors for  
promoter/enhancer analysis in Drosophila  
JOURNAL Biotechniques 29 (4), 726-728 (2000)  
MEDLINE 20510562  
PUBMED 11056799  
REFERENCE 2 (bases 1 to 10020)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall /  
9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
REFERENCE 3 (bases 1 to 10020)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall /  
9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
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SOURCE Stinger GFP transformation vector.  
ORGANISM Stinger GFP transformation vector  
artificial sequence; vectors.  
REFERENCE 1. (bases 1 to 10095)  
AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.  
TITLE GFP and beta-galactosidase transformation vectors for  
promoter/enhancer analysis in Drosophila  
JOURNAL Biotechniques 29 (4), 726-728 (2000)  
MEDLINE 20510562  
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REFERENCE 2 (bases 1 to 10095)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall /  
9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
REFERENCE 3 (bases 1 to 10095)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
TITLE Direct Submission  
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9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
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DEFINITION Green H-Pelican GFP transformation vector, complete sequence.

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VERSION AF242363.2 GI:12237301

KEYWORDS .

SOURCE Green H-Pelican GFP transformation vector.

ORGANISM Green H-Pelican GFP transformation vector

REFERENCE 1 (bases 1 to 10189)

AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.

TITLE GFP and beta-galactosidase transformation vectors for promoter/enhancer analysis in Drosophila

JOURNAL BioTechniques 29 (4), 726-728 (2000)

MEDLINE 20510562

PUBMED 11056799

REFERENCE 2 (bases 1 to 10189)

AUTHORS Barolo,S.E. and Posakony,J.W.

TITLE Direct Submission

JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA

REFERENCE 3 (bases 1 to 10189)

AUTHORS Barolo,S.E. and Posakony,J.W.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA

REMARK Sequence update by submitter

COMMENT On Jan 16, 2001 this sequence version replaced gi:9754907.

FEATURES

Location/Qualifiers

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AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.  
TITLE GFP and beta-galactosidase transformation vectors for promoter/enhancer analysis in Drosophila  
JOURNAL BioTechniques 29 (4), 726-728 (2000)  
MEDLINE 20510562  
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AUTHORS Barolo,S.E. and Posakony,J.W.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA  
REFERENCE 3 (bases 1 to 10288)  
AUTHORS Barolo,S.E. and Posakony,J.W.  
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RESULT 10

AF242360

LOCUS AF242360 13336 bp DNA circular SYN 16-JAN-2001

DEFINITION Pelican lacZ transformation vector, complete sequence.

ACCESSION AF242360

VERSION AF242360.2 GI:12237286

KEYWORDS .

SOURCE Pelican lacZ transformation vector.

ORGANISM Pelican lacZ transformation vector

REFERENCE 1 (bases 1 to 13336)

AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.

TITLE GFP and beta-galactosidase transformation vectors for promoter/enhancer analysis in Drosophila

JOURNAL Biotechniques 29 (4), 726-728 (2000)

MEDLINE 20510562

PUBMED 11056799

REFERENCE 2 (bases 1 to 13336)

AUTHORS Barolo,S.E. and Posakony,J.W.

TITLE Direct Submission

JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA

REFERENCE 3 (bases 1 to 13336)

AUTHORS Barolo,S.E. and Posakony,J.W.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA

REMARK Sequence update by submitter

COMMENT On Jan 16, 2001 this sequence version replaced gi:9754904.

FEATURES

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DEFINITION H-Pelican lacZ transformation vector, complete sequence.

ACCESSION AF242361

VERSION AF242361.2 GI:12237291

KEYWORDS

SOURCE H-Pelican lacZ transformation vector.

ORGANISM H-Pelican lacZ transformation vector

REFERENCE 1 (bases 1 to 13508)

AUTHORS Barolo,S., Carver,L.A. and Posakony,J.W.

TITLE GFP and beta-galactosidase transformation vectors for promoter/enhancer analysis in Drosophila

JOURNAL Biotechniques 29 (4), 726-728 (2000)

MEDLINE 20510562

PUBMED 11056799

REFERENCE 2 (bases 1 to 13508)

AUTHORS Barolo,S.E. and Posakony,J.W.

TITLE Direct Submision

JOURNAL Submitted (08-MAR-2000) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA

REFERENCE 3 (bases 1 to 13508)

AUTHORS Barolo,S.E. and Posakony,J.W.

TITLE Direct Submision

JOURNAL Submitted (16-JAN-2001) Biology, U.C. San Diego, 4121 Bonner Hall / 9500 Gilman Dr., La Jolla, CA 92093-0349, USA

REMARK Sequence update by submitter

COMMENT On Jan 16, 2001 this sequence version replaced gi:9754905.

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QY 6172 atctgtgtgaaatcttaataagggtccaaattaccaaattgaaactcagtttgcggcgctg 6231

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Db 2708 GGCCTCATCTTTTGGGCCCAACAACCTCACGCAAGTGGCGGTGATGAATATCAACGGAGCC 2767

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Db 2768 ATCTTCCCTCTTCTTGACCAACATGACCTTTCAAAACGCTCTTTGCCACGATAAATGTAAGT 2827

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Db 3068 CTTCAACTGCCCTGGCGTGGTCACTCTGGTGGCCAAATGTGTCAACGTCTCTTCGGATATCT 3127

QY 7911 aatacctgcgccagctcctcgacctcgatggcgctgtcgtgggtccgcggttatcat 7970

Db 3128 AATATCCTGCGCCAGCTCCTCGACCTCGATGGCGCTGTCTGTGGGTCCGCCGGTTATCAT 3187

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Qy	9045	aggattagcagagcgaggtatgttagcggtgctacagagttcttgaagtggtggcctaac	9104
Db	5468	AGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC	5527
Qy	9105	tacggctacactagaaaggacagttatttgggtatctcggtctctgctgaagccagttaccttc	9164
Db	5528	TACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC	5587
Qy	9165	ggaaaaagagtttggtagctcttgatccgggcaaaaaccaccgcgtggtagcgggtgtttt	9224
Db	5588	GGRAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAACCACCGCTGGTAGCGGTGTTT	5647
Qy	9225	tttgtttgcaagcagcagattacgcgcagaaaaaaaggtatctcaagaagatccctttgatc	9284
Db	5648	TTTGTTTGCAAGCAGCAGATTACGGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC	5707
Qy	9285	ttttctacggggtctgacgctcagtggaacgaaaaaactcacgttaagggatttggtcatg	9344
Db	5708	TTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGTCATG	5767
Qy	9345	agattatacaaaaaggatcttcacctagatccctttaaaaataaaaaagaagttttaaataca	9404
Db	5768	AGATTATCAAAAAGGATCTTCACCTAGATCCTTTAAATTAAAAATGAAGTTTAAATCA	5827
Qy	9405	atctaaaagtatatatgagtaaaacttggctgacagttaccaatgcttaataatcagtgagcoa	9464
Db	5828	ATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGCA	5887
Qy	9465	cctatctcagcgatctgtctatttctgttcacatagttgcctgactcccccgctcgtgtag	9524
Db	5888	CCTATCTCAGCGATCTGCTCTATTTCGTTTCATCCATAGTTGCCTGACTCCCCCGTGTAG	5947
Qy	9525	ataactacgatacgggagggttaccatctggccccagtgctgcaatgataccgcgcgagac	9584
Db	5948	ATAACTACGATACGGAGGGCTTACCATCTGCCCCCAGTGCTGCAATGATACCCGGAGAC	6007
Qy	9585	ccacgctcacgggtccagatttatcagcaataaaaccagccagccggaaggccgagcgc	9644
Db	6008	CCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGCCGAGCGC	6067
Qy	9645	agaaagtggtcctgcaactttatccgcctccatccagttctattaattgttgcggggaagct	9704
Db	6068	AGAAGTGGTCCCTGCAACTTTATCCGCCCTCCATCCAGTCTATTAAATTGTTGCCGGAAGCT	6127
Qy	9705	agagtaagtagttcgccagtttaatatgttgcgcaacggttgttgccattgctacaggcatc	9764
Db	6128	AGAGTAAGTAGTTGCCCAGTTAATAGTTTGCGAACGTTGTTGCCATTGCTACAGGCATC	6187
Qy	9765	gtggtgtcacgctcgtctgttgggtatggcttcattcagctccggttccccaacgatcaagg	9824
Db	6188	GTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGCTTCCCAACGATCAAGG	6247
Qy	9825	cgagttacatgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatc	9884
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Qy	9885	gttgtcagaagtaagttggccgcagtggttatcactcatggttatggcagcactgcataat	9944
Db	6308	GTTGTCAAGATAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAAT	6367
Qy	9945	tctcttactgtcatgccatcccgtaagatgcttttctgtgactggttgactactcaaccaag	10004
Db	6368	TCCTCTTACTGTCAATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAG	6427
Qy	10005	tcattctgagaatagtgtatcgcgccagcagttgtctcttgcggcgctcaacacgggat	10064
Db	6428	TCAATTCTGAGAAATAGTGTATGCGGGGACCGAGTTTGCTCTTGCCCCGGCGTCAATACGGGAT	6487
Qy	10065	aataccgcgcacatagcagaactttaaaagtgtcatcatcttggaataacgttcttcgggg	10124
Db	6488	AATACCGGCCACATAGCAGAACTTTAAAAAGTGCTCATCATGTGGAACCGTTCTTCGGGG	6547

Qy	10125	cgaaaaactctcaaggatctttacocgctgttgagatccagttcogatgtaacccactcgtgca	10184
Db	6548	CGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAAACCCACTCGTGCA	6607
Qy	10185	cccaactgatcttcagcatcttttactttccaccagcgtttctgggtgagcaaaaacagga	10244
Db	6608	CCCAACTGATCTTCAGCATCTTTTACTTTCAACCAGCGTTTCTGGGTGAGCAAAAACAGGA	6667
Qy	10245	aggcaaaatgcgcgcaaaaaagggaataaaggcgacacggaatgttgaatactcatactc	10304
Db	6668	AGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTC	6727
Qy	10305	ttcctttttcaaatatttgaagcatttatcaggggttatgttctcatgagcggatacata	10364
Db	6728	TTCCCTTTTCAATATTTTGAAGCATTTATCAGGGTTATTGTTCTCATGAGCGGATACATA	6787
Qy	10365	tttgaatgtatttagaaaaataaacaataaggggttccgcgcacatttccccgaaaaagt9	10424
Db	6788	TTTGAATGTATTTAGAAAAATAAACAATAAGGGTTCCCGCGCACATTTCCCCGAAAAAGTG	6847
Qy	10425	ccacctgacgtctaaagaaaccattattatcatgacattaaacctataaaaaataggcgtatc	10484
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Qy	10485	acgagcccttctcgtctcgcgcggttctcgggtgatgacggtgaaaaacctctgacacatgcag	10544
Db	6908	ACGAGGCCCTTTCGTCTCGCGCGGTTCGGGTGATGACGGTGAACCCCTCTGACACATGCGAG	6967
Qy	10545	ctcccgagagacgggtcacacagcttgtctgtaagcggatgcgggagcagacaagcccgctcag	10604
Db	6968	CTCCCGGAGACGGTCAACAGCTTGTCTGTAAAGCGGATGCCGGGAGCAGACAAGCCCGTCAG	7027
Qy	10605	ggcgcgtcagcggggtgttgcggggtgtcggggctggcttaactatgcggcatcagagcag	10664
Db	7028	GGCGCGTCAGCGGGTGTGGCGGGTGTCTGGGGTGGCTTAACTATCGGCGATCAGAGCAG	7087
Qy	10665	attgtactgagagtgcaccatatgcggtgtgaaatacgcgcaaccggaatcgcggaactaa	10724
Db	7088	ATTGTACTGAGAGTGCACCATATCGGTTGTGAAATACCGCACCGGAATCGCGCGGAACATAA	7147
Qy	10725	cgacagtcgctcccaaggtcgtcgaacaaaaagtgtaagtgttcgagagcggttgggag	10784
Db	7148	CGACAGTCGCTCCAAGGTCGTGAAACAAAAGGTGAATGTGTGCGGAGAGCGGTGGGAG	7207
Qy	10785	acagcgaagagcaactcgaacacgtggtgtggtgaggtgaaattatgaagagggcgcg	10844
Db	7208	ACAGCGAAAGAGCAACTACGAAACGTTGGTGTGGTGGAGGTGAATTATGAAGAGGGCGCGC	7267
Qy	10845	gattgaaaaagtatgtatataaaaaatatatcccggtgttttatgtagcgaataaacgagt	10904
Db	7268	GATTTGAAAAAGTATGTATATAAAAAATATATCCCGGTGTTTTATGTAGCGATAAACGAGT	7327
Qy	10905	ttttgatgtaagggtatgcagggtgtgtaagtcctttcggttagaagacaaaatccaaaagtcta	10964
Db	7328	TTTTGATGTAAGGTATGCAGGTGTGTAACTCTTTTGGTTAGAAGACAAATCCAAAAGTCTA	7387
Qy	10965	cttggtggggtgttcgaaggggaaaaatacttgtaattctataggtcatatcttgtttttatt	11024
Db	7388	CTTGTTGGGATGTTTCGAAGGGGAAATACTTGTATTCTATAGGTCTATCTTGTTTTATT	7447
Qy	11025	ggcacaaaataataattacattagctttttgagggggcaataaaacagtaaacacgatggttaa	11084
Db	7448	GGCACAATAATAATTACATTAGCTTTTTTGAAGGGGCAATAAAACAGTAAACACGATGGTAA	7507
Qy	11085	taatggtaaaaaaaacaagcagttatttcggatatatatgtcggctactccttgcgtcg	11144
Db	7508	TAATGGTAAAAAAAACAAAGCAGTTATTTCGGATATATGTCCGCTACTCCTTGGCTCG	7567
Qy	11145	ggccccgaagtcttagagccagatatgcgagcccccgaagctcacgatgagaatggcccag	11204
Db	7568	GGCCCCGAAGTCTTAGAGCCAGATATGCGAGCACCCCGGAAGCTCACGATGAGAATGGCCAG	7627



Db	1154	GGCCAAC	TAGCCGAGAACCTCACCTATGCTTGGCACAATATGGACATCTTTGGGGCGGTC	1213
QY	6044	aatcagccgggctccggatg	gcggcagctggtcaaccggacacgcggaactattctgcaac	6103
Db	1214	AATCAGCCGGGCTCCGGATGGCGCAGCTGGTCAACCGGACACGGGACTATTCTGCAAC	1273	
QY	6104	gagcgacacataccggcgcccgaggaacatttgctcaagaa	cggtaggtgagtttctattcgca	6163
Db	1274	GAGCGACACATACCGCGCGCCAGGAACATTTGCTCAAGAACGGTGAGTTTCTATTTCGCA	1333	
QY	6164	gtcggctgatgtgtgaaatcttaataaagggtccaattacc	aaattgaaactcagttt	6223
Db	1334	GTCGGCTGATCTGTGTGAAATCTTTAATAAAGGGTCCAATTACCAATTTGAAACTCAGTTT	1393	
QY	6224	gcggcgtggccctatccgggcgaaacttttggccgtgat	ggcgagttccgggtccgggaaga	6283
Db	1394	GCGGCGTGCCCTATCCGGGGCAACTTTTGGCCGTGATGGGCAGTTCCGGTGCCGGAAAGA	1453	
QY	6284	cgaccctgctgaatgccccttgccctttcgatcgccgcag	ggcatcccaagtatcgccatccg	6343
Db	1454	CGACCCCTGCTGAATGCCCTTGCCCTTCGATCGCCGAGGGCATCCAAGTATCGCCATCCG	1513	
QY	6344	ggatgcgactgctcaatggccaaaccttgacccctcttat	ggcctccctaa	6403
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QY	6404	atgtccagcaggatgacctctttatggcctccctaa	cggccagggaacacctgatcttc	6463
Db	1574	ATGTCCAGCAGATGACCTCTTTATCGCTCCCTAACGGCCAGGAACACCTGATTTTCC	1633	
QY	6464	aggccatggtgcggatgccacgacatctgacctatcg	cgcagagtgccccgcgtggtc	6523
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QY	6524	agtgatccaggagctttcgctcagcaaatgtcagca	cacagatcgcgtgtgccccggca	6583
Db	1694	AGGTGATCCAGGAGCTTTCGCTCAGCAANAATGTCAGCACACGATCATCGGTGTGCCCGGCA	1753	
QY	6584	gggtgaaagttctgtccggcgagaaagcgtctg	gcattcgccctccgaggcaactaa	6643
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QY	6644	ccgatccgcgcttctgatctgcgatgagccacccac	ctccggactggactcatttaccgcc	6703
Db	1814	CCGATCCGCGCTTCTGATCTGCGATGAGCCCA	CCCTCCGACTGGACTCATTTACCGCC	1873
QY	6704	acagcgtcgtccaggtgctgaagaagctgtcgaga	agggaagcagcgtcatcctgacca	6763
Db	1874	ACAGCGTCGTCCAGGTGCTGAAGAAGCTGTGCGAGAAGSGCAAGACCGTCACTCCTGACCA	1933	
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Db	1934	TTCATCAGCGCTCTTCCGAGCTGTTTGAGCTCTTTGACAAGATCCTTCTGATGGCCGAGG	1993	
QY	6824	gcagggtagcttcttgggcactcccagcgaagccg	tcgacttctttcctagtgttc	6883
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QY	6884	gatgtgttattaagggtatctagcattacattacat	ctcctaactcctatccagcgtgggt	6943
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QY	6944	gcccagtgctotaccaactacaatccggcgggact	ttttacgtacaggtgttgccgtgtg	7003
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QY	7004	cccggacgggagatcgagtc	ccgtgatcgatcgccaagatatcgacaaattttgctatt	7063
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QY	7064	agcaaatgagccccggatatggagcagttgttgg	ccacccaaaaatttggagaagccactg	7123
Db	2234	AGCAAAGTAGCCCCGGGATATGGAGCAGTTGT	TGGCCACCAAAAAATTTGGAGAAGCCACTG	2293

QY	7124	gagcagccgggagaatgggtacacacctacaaggg	ccacctggttcatgcagttccgggcgggtc	7183
Db	2294	GAGCAGCCGGAGAATGGGTACACCTACAAGG	CCACCTGGTTCATGCGAGTCCGGGGCGGTC	2353
QY	7184	ctgtggcgatcctggctgctggtgctcaagga	accactcctcgtaaaaagtcgcacttatt	7243
Db	2354	CTGTGGCGATCCTGGCTGTGCGTGCTCAAG	GAACCACTCCTCGTAAAAAGTTCGACTTATT	2413
QY	7244	cagacaaacggtgagtggttccagtggaacaa	aatgatataacgcgttacaaattcttgga	7303
Db	2414	CAGACAAACGGTGAGTGGTCCAGTGGAA	ACAAATGATATAACGCTTACAATTTCTTG	2473
QY	7304	caaatcgctagattttagttagatggaattg	cctgattccacaccccttcttagtttttcaa	7363
Db	2474	CAAATTCGCTAGATTTAGTTAGATTGCC	TGATTCCACACCCCTCTCTTACTTTTCAA	2533
QY	7364	tgagatgtatagtttatagtttgcagaaaa	ataataaatttcatttaactcgcgaacat	7423
Db	2534	TGAGATGTATAGTTTATAGTTTTCAG	AAAAATTAATTTCAATTTAACTCGGAACAT	2593
QY	7424	gttgaagatatgaatatattaatgagatgc	gagtaaacattttaatttgcagatggttgccat	7483
Db	2594	GTTGAAGATATGAATATTAAATGAGAT	GCGAGTAACATTTTAATTTGCAGATGGTTGCCAT	2653
QY	7484	cttgattggcctcatcttctcctgacca	aacatgaccttcaaaacgtctttgccacgataa	7543
Db	2654	CTTGATTGGCCTCATCTTTTGGGCCA	CAACTCACGCAAGTGGCGTGATGAATATCAA	2713
QY	7544	cggagccatcttctcctgacca	aacatgaccttcaaaacgtctttgccacgataa	7603
Db	2714	CGGAGCCATCTTCCCTCTCCTGACCA	ACATGACCTTTCAAAACGCTTTTGCCACGATAA	2773
QY	7604	tgtaagtcctgtttagaatacatttgca	tatttaataatttactaaactttctaataatcg	7663
Db	2774	TGTAAGTCTTGTTTGAATACATTTGC	ATATTAAATAATTTACTAACITTTCTAATGAATCG	2833
QY	7664	attcgatttaggtgttcacctcagagctgc	cagtttttatgagggaggcccggaagtcgac	7723
Db	2834	ATTGGAATTTAGGTGTTCACTCAGAG	CTGCCAGTTTATGAGGGAGGCCCGGAAGTCGAC	2893
QY	7724	tttatcgtgtgacacatacttctctggg	caaaaacgatggccgaattaccgcgttttctca	7783
Db	2894	TTTATCGCTGTGACACATACTTTCT	TGGCAAAACGATTGCCGAATTAACCGCTTTTCTCA	2953
QY	7784	cagtgccactggtcttcacggcgattgc	ctatcgcgatgcggactgcggcgagtcg	7843
Db	2954	CAGTGCCACTGGTCTTCACGGCGATT	TGCCATTCGGTGGCCAAATGTGTCAACGTCCTTCG	3013
QY	7844	tgcaacttctcaactgcctggcgtggtc	actctggtggccaatgtgcaacgctcctcg	7903
Db	3014	TGCACCTTCTCAACTGCTGGCGTG	GTCACTGCTGGTGGCCAAATGTGTCAACGTCCTTCG	3073
QY	7904	gatatctaatactcctgcgcagctcct	cgacctcgatggcgtgctgtggtggtccgcgg	7963
Db	3074	GATATCTAATATCCTCGCCACGCT	CCTCGACCTCGATGGCGCTGTCTGTGGGTCCGCCCGG	3133
QY	7964	ttatcatacattcctgctcttggcggt	cttcttllgaactcgggctcgggtgccaagtat	8023
Db	3134	TTATCATACCATTCCTGCTCTTTTGG	CGGCTTCTTCTTGAACCTCGGGCTCGGTGCCAGTAT	3193
QY	8024	acctcaaatggttgctgtacctctcat	ggttccgttacccaaacgaggtctgtgatta	8083
Db	3194	ACCTCAAATGGTTGTGTACCTCTCA	TGTTCCGTACGCCAACGAGGCTGTGCTGATTA	3253
QY	8084	accaatgggcggacgtggagccgggcg	aaaaattagctgcacatcgtcgaacacccacgtgcc	8143
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Db	3314	CCAGTTCGGGCAAGGTTCATCTCTG	GAGACGCTTAACTTCTCCGCCCGCCGATCTGCCGCTGG	3373



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QY	9278	tttgatcttttctacggggtctgcagctcagtggaacgaaaaactcaactgaaggatttt	9337
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QY	9338	ggtcatgagattatcaaaaaaggatcttcacactagatcccttttaataataaaatgaagt	9397
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Db	5774	TAAATCAATCTAAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAG	5833
QY	9458	tgaggcacctatctcagcgatctgtctatttctgttcattccatcgaagtgcctgactccccgt	9517
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QY	9518	cgtgtagataactacgatacgggagggcttaccatctggccccagtgctgcaatgatacc	9577
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QY	9758	aggcatcgtggtgtcacgctcgtcgtttgggtatggcttcattcagctccggttccccaacg	9817
Db	6134	AGGCATCGTGGTGTACAGCTCGTCTGTTGGTATGGCTTCATTACGCTCCGGTTCCCCAACG	6193
QY	9818	atcaaggcgaggtacatgatccccccatggttgcaaaaaagcggttagctccttcggtcc	9877
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QY	9878	tccgatcgttgtcagaagtaagttggccgcagtggttatcactcatggttatggcagcaact	9937
Db	6254	TCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCATTCTATGGTTATGGCAGCACT	6313
QY	9938	gcataaattctctactgtcatgccatccgtaagatgcttttctgtgactggtgagtactc	9997
Db	6314	GCATAATTCTCTTACTGTCTATGCCATCCGTAAAGATGCTTTTCTGTGACTGGTGAGTACTC	6373
QY	9998	aaccaagtcattctgagaatagtgatcgcgccagcttgctcttgcggcgctgaac	10057
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QY	10058	acgggataataccgcgcacacatagcagaactttaaaagtgctcatcatggaaaaagcttc	10117
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QY	10178	tcgtgcacccaactgatcttcagcatctttactttaccagcgtttctgggtgagcaaaa	10237
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QY	10538	catgcagctccccggagacggtcacagcttctgtctaagcggatgccgggagcagacaagc	10597
Db	6914	CATGCAGCTCCCGGAGACGGTCAAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGC	6973
QY	10598	cgtcagggcgctcagcgggtgttgcggggtgtcggggtggttaactatgcggcatc	10657
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QY	10658	agagcagattgtactgagagtgccaccatatgcgggtgtgaaataccgcacccaatcgcgcg	10717
Db	7034	AGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCCACCGAATCGCGCG	7093
QY	10718	gaactaacgacagtcgctccaaaggtcgtcgaacaaaagggtgaatggttcgggagagcgg	10777
Db	7094	GAACTAACGACAGTCGCTCCAAGTCTGTCGAACAAAAAGGTGAATGTGTTGCGGAGAGCGG	7153
QY	10778	gtgggagacagcgaagagcgaactacgaaacgtggtgtggtgaggtgaattatgaagag	10837
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QY	11138	tcgctcggggcccgaaagtcttagagccagatatgcgagcaccgggaagctcacgatgagaa	11197
Db	7514	TGCGTCGGGCCCGGAAGTCTTAGAGCCAGATATGCAGCACCCCGGAAGCTCACGATGAGAA	7573
QY	11198	tgggccagac 11206	
Db	7574	TGGCCAGAC 7582	
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RESULT	14		
DMCASPER1			
LOCUS	DMCASPER1	7775 bp	DNA linear SYN 29-APR-2000
DEFINITION	D.melanogaster P element CaSper-1 gene.		
ACCESSION	X81644		
VERSION	X81644.1 GI:551447		
KEYWORDS	Carnegie-4 vector; P element; transformation vector; white gene.		





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RESULT 15

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LOCUS

DEFINITION P element transformation vector pCaSper-3, complete sequence.

ACCESSION U59055

VERSION U59055.1 GI:1432062

KEYWORDS

SOURCE

ORGANISM

P element transformation vector pCaSper-3.

P element transformation vector pCaSper-3

artificial sequence; vectors.

REFERENCE 1 (bases 1 to 7815)

AUTHORS Thummel,C.S. and Pirrotta,V.

TITLE New pCaSper P element vectors

JOURNAL Dros. Info. Service 71, 150-150 (1992)

REFERENCE 2 (bases 1 to 7815)

AUTHORS Thummel,C.S. and Pirrotta,V.

TITLE Direct Submission

JOURNAL Submitted (23-MAY-1996) Human Genetics, Univ. of Utah, Bldg. 533, Salt Lake City, UT 84112, USA

FEATURES

source

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misc\_feature

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